

09405504.092399

mmFATP1	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mmFATP2	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mmFATP3	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mmFATP4	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mmFATP5	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
ceFATPa	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
scFATP	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mtFATP	1	-----HRAADGAGNAEIVASLALLWFLQLPMTWANAANFCVYVGGGCGSRFLNIVCTARRDLFQLSVLR
mmFATP1	64	YVLELRRHRAAGDTIPCFQAVARRQPERALALVDS-----GICWTFACOLDYSSNAVAFALRQLGGT---
mmFATP2	41	HRVRSYRORRPVYILRAFLERQARKTHHPTFLFR-----DETLYAQLVDRNSQVYALRHLHDQLG---
mmFATP3	35	QNFSTAAEAAREGRIARALR-ANGWTGGRGSGR-----GSTEELARVAPPAGDAAAGATTAPP---
mmFATP4	74	YFRRLNLWHPHNVDALEERQALAWPRAVALVCTG-----HASTHMS-----
mmFATP5	63	VNIDWWRLKQNKCHHELFLDVIKRGHRAAMIDIE-----SESSITSSOLDARSCQAAHVNAKLLKDAY
ceFATPa	74	VFCYIDVRRHFPONWYFLIKQYQCGHLMISYTRPHAKEGFELETFTTYTNTYVLRSLHILHFDYN---
scFATP	64	ANTGLARPNKAKISGTYFOEDRANAYGRVFLKFG-----DQQLTRDANANRYNAVLAAARG---
mtFATP	35	-----DQQLTRDANANRYNAVLAAARG---
mmFATP1	126	---AGGVVAVFLGKRFVVGWLOLAKAGVVAALLVNRERELNFCGCTSAKALITYCENAAAVAEVSP
mmFATP2	101	---LROGQVAVLIGNHPHYVWLOLAKAGVVAALLVNRERELNFCGCTSAKALITYCENAAAVAEVSP
mmFATP3	94	---LROGQVAVLIGNHPHYVWLOLAKAGVVAALLVNRERELNFCGCTSAKALITYCENAAAVAEVSP
mmFATP4	8	---LROGQVAVLIGNHPHYVWLOLAKAGVVAALLVNRERELNFCGCTSAKALITYCENAAAVAEVSP
mmFATP5	140	IQNTKDAAMTLLPSKTSALSVLGLAKLGLCPVAVWISRLRNDLRRHCLKALALIFGSEMAAALVSH
ceFATPa	125	---SGDYVALLTNNNSHTVAWGLAGLIGVTAWISRLRNDLRRHCLKALALIFGSEMAAALVSH
scFATP	134	---VQMDVVAIDCTFARALR-ANGWTGGRGSGR-----GSTEELARVAPPAGDAAAGATTAPP---
mtFATP	94	---VQMDVVAIDCTFARALR-ANGWTGGRGSGR-----GSTEELARVAPPAGDAAAGATTAPP---
mmFATP1	195	GLKMLLFCSSDLPKPSLFPDOLLPPLAARATTPAAGARQ-----GDRLLFYITTSOTGLPKAAIVVSH
mmFATP2	171	TLK---KDAVSVVY---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
mmFATP3	164	ALR---AMGLHLMAT---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
mmFATP4	56	SLRFLSLFCSSDLPKPSLFPDOLLPPLAARATTPAAGARQ-----GDRLLFYITTSOTGLPKAAIVVSH
mmFATP5	213	MLR---AENHICF---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
ceFATPa	194	OKLFYDYEOTEVYSY---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
scFATP	204	OKLFYDYEOTEVYSY---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
mtFATP	164	SRG---RVV---GRTSTNGVDTLDKVGVGVSPTFLVRSSEVFTTPAVYITTSOTGLPKAAIVVSH
mmFATP1	265	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mmFATP2	241	RLRYDGLG-LAMISGITLA---QDVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mmFATP3	234	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mmFATP4	125	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mmFATP5	283	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
ceFATPa	264	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
scFATP	273	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mtFATP	223	RYVRIANFGHSYSRRA---ADVLYDCLFLYHSAGLHGVGGCVYVOLTYYLRRKFSASRFPWDDCYVYECTVVQ
mmFATP1	336	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mmFATP2	311	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mmFATP3	304	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mmFATP4	196	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mmFATP5	353	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
ceFATPa	353	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
scFATP	344	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mtFATP	295	YIGEXCYLLCQPYRVDORHVRVLAONGLRPAIWRERFORFGVPOIGEFYATECNCISLANNDDQR---VOS
mmFATP1	406	COYF---SRLLT---YPIRLVXVNDNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mmFATP2	381	VOIRA---NYLQK---VARTYLIHVDKNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mmFATP3	374	VOIRA---NYLQK---VARTYLIHVDKNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mmFATP4	266	COYF---SRLLT---YPIRLVXVNDNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mmFATP5	423	VOIRA---NYLQK---VARTYLIHVDKNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
ceFATPa	404	COYF---SRLLT---YPIRLVXVNDNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
scFATP	417	COYF---SRLLT---YPIRLVXVNDNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mtFATP	365	COYF---SRLLT---YPIRLVXVNDNEFV---ADSEGLCIPGQOPRGLLVQIIN---QODPFRFPGVY---GDSAT
mmFATP1	473	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mmFATP2	446	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mmFATP3	439	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mmFATP4	333	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mmFATP5	488	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
ceFATPa	473	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
scFATP	489	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mtFATP	423	KKKTAHSVFRKGSATLGGDYLVNDLGGHYFRDRSGDTFRWKGENVSTTEVAVVGL---LGLQTDVAVTGVV
mmFATP1	544	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mmFATP2	517	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mmFATP3	510	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mmFATP4	404	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mmFATP5	559	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
ceFATPa	544	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
scFATP	562	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mtFATP	494	VPGVEKAGNAALADHSOLDPMS---NYQFQIAXV-LASTARPIFLRLPQVDTTGTFTIQTALLOREGFD
mmFATP1	611	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
mmFATP2	585	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
mmFATP3	578	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
mmFATP4	471	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
mmFATP5	627	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
ceFATPa	616	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
scFATP	616	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---
mtFATP	562	PRQISDRLFLFLDLAGQNYVPLDPAVHARTCAGDPSL---

Figure 1

Fig. 2A

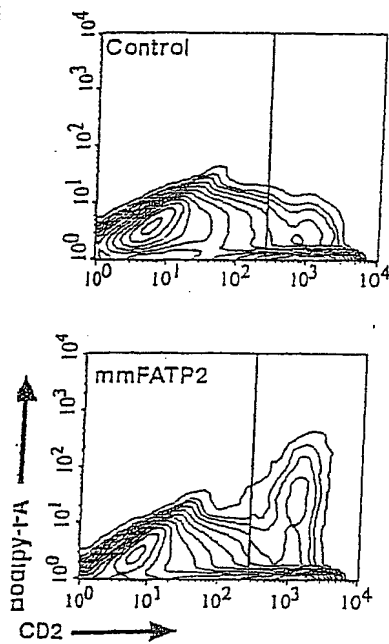


Fig. 2C

Fig. 2B

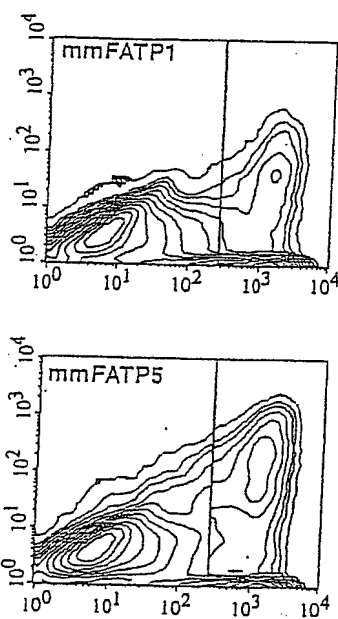


Fig. 2D

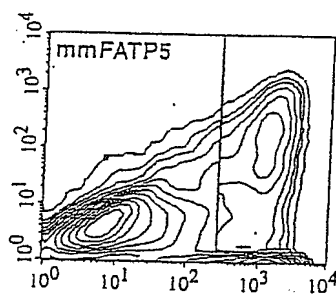


Fig. 3

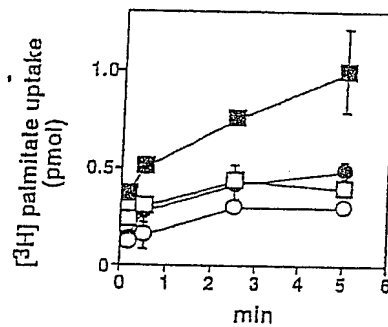
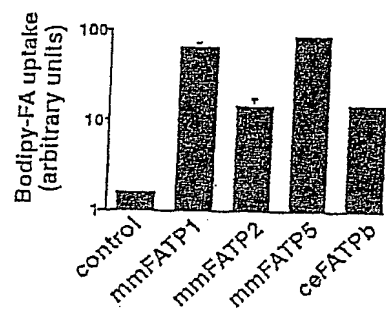


Fig. 4

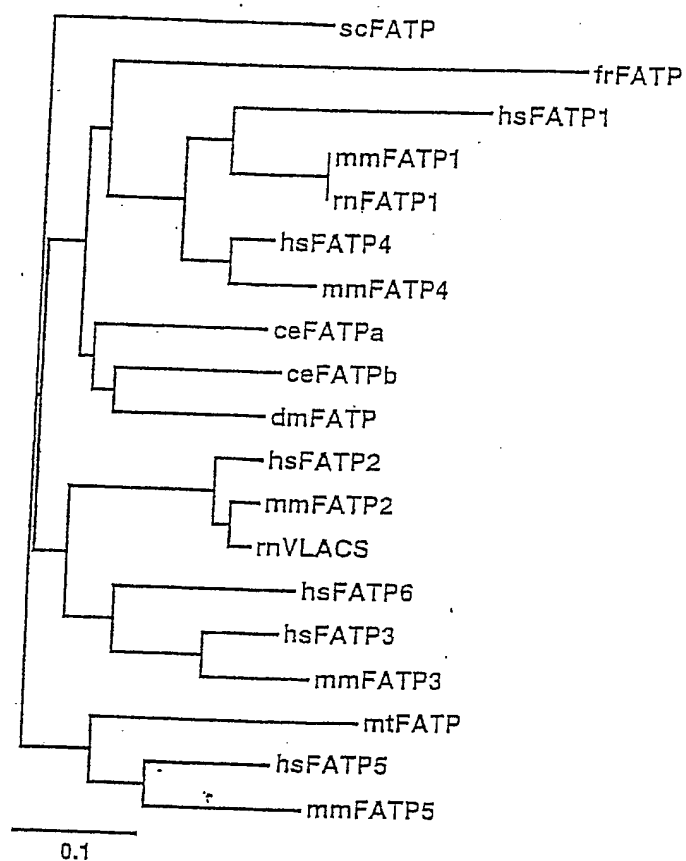


Figure 5

FIG. 6

246	FIFTSGTTGLPKPAILLSHERRVIOVSNVLSFCGCR--ADDVVVDVLEPLVHTITGLVLGFLGLQVGGATCVLAPKFSASRFWAECRQHGVTVI	mmEATP1
265	VVYTSGETTGNPKPAVIKHFPMFWL--AMCAGKAFGINKSDVVYITMPMVHSAAGIMGTGLIAFGSTAVIRKKFSASNEWKDCVKYNVITAT	mmFATP5
249	-LYTSGTNGGLPKSATMSWRKSSVGCQVFG-HVHMTNSETVFTAMPLFHSSTAALFGACALSHGGCLATSHKFSASTFWKQVYLITGATHH	ceFATPa
256	YLYTSGTTGLPKAAIVVHSRYRIL--AAFGHHSYSMRAADVLXDCPLVHSAGNEMGVQCQVIYGLHVIRKKFSASRFDWDDGVKXNCIVV	SCFATP
205	YIFTSGTTGFPKASVMTHRWLRALAVFGGMGLRLKGSDTLYSCPLVYHNALTVAVSSVINSGATIALGKFSASRFDWDEVIANRATAF	mtFATP
100	110 120 130 140 150 160 170 180	
335	QYIGETICRYLHROPVRDVEQRHRVRLAVNGGLRPAIWEFTQREFGVPOIGEFYCATTEC--NCSHANMKGKVGSCGFNSRLLTHV---YP	mmFATP1
353	LYVGEILLRVHCNVEQPEDKIHTVRLAMGTGLRANVWKNFQORFGPIRIWEFYGSTEG--NVGLMNY---VGHGGAVGRFTSCILRLMLTP	mmFATP5
338	QYIGETICRYLLAANPCPEEKQHNVRMLWNGGLRGQIWKKEFVGRFGIKKIGELVYSTEG--NSNIVNVVDNHVGACGFMP--HYPHIGSLYP	ceFATPa
345	QYVGEVCRVILHTEISKYEKMHKVKVAYGNGGLREDIWDQRKRFNIEVIGEFMAATEAPFATTFOKDFGIGAGRNYGTIIQWF--ISFQ	SCFATP
295	VYIGETICRYLHNOBAKETDRAHQVRVICGNGGLRPEIWDDEFTTREFGVARVCEFFVAASEG--NSAFINI---F---NVPRTAGVSPM---P	mtFATP
190	200 210 220 230 240 250 260 270	
419	TRLVKVNEDTMEPL--RDSSEGLCTPCQGEPLGLVGOIN--QDDPLRRREDGVV--SDSATNKKLAHSVERKGBSAYLSGDDVLMDEELGVMYER	mmFATP1
437	FELVQFDIETAEPL--RDKQGFCTPVPEPGKPGLLLTQVR--KNQP---FLGYRGSQAEASNRKINVANVRVGEDLYENTGDVLTLDQEGFFYEQ	mmFATP5
424	VRLIKVDRATGELE--RDKNGLCVPCVPGETGEMVGVIK--EKDILLKEEGVV--SEGDTAKKIYRDVFKHGDVKVFAAGDILHWDLDLGYLVFV	ceFATPa
434	QTLVRMDPNDDSVIYRNSKGFCEVAPVGEPEGEMMRIFFPKBPETSEFQGLGNAKETKSKVVRDVERFGDANYRCGDLAKADFYGLWYEL	SCFATP
373	LAFVEYDLDTGDPL--RDASGRVRRVPDGEPLLSRVN--RLQP---FDGYTDP--VASEKKLVRNAFRDGCWENTGDVMSPOGMGHAAFY	mtFATP
280	290 300 310 320 330 340 350 360	
506	DRSGDTERWRGENVSTTEVEAVLSRLGQT--DVAVVGVAVPVGEKGAGMAATADPHS--QLDP--NSMYQELQK--VLAASYARPIELR	mmFATP1
522	DRIGDTERWKGENVSTGEVECVLSSLDFLK--EVNVVGVPVPGCEGKVGMAAVKLPAGK--TFDG--KKLYQHVRIS--WEPAYATPHEIR	mmFATP5
511	DRCGDTERWKGENVSTTEVEGILEQPVMDVE--DATVVGVTGKMEGRAGMAGIVVKDGT--DVEKFIADITSRTE--NLASVAILRVEIR	ceFATPa
524	DRMGDTERWKSENVSTTEVEDQLTASNKEQYAOVLVVGKVPKYEGRAGFAVIKLTDNSLDITAKTKLENDSLSRLNHEPSYAMPFLVK	SCFATP
457	DRLEDTERWKGENVATIQVEAALASDQTV--ECTVYGVQIPRTGGRAGMAATILRAGA--EFDG--QALARTVYG--HLPGYALPLFVR	mtFATP

mmFATP3 DNA sequence

ACGACTCACTATAGGGAGACAGCCTATGACGTGGCATGCAC 40
GCGTAAGCCTTGGGCCCCCTGAGGCATCCCTAGAGGGCCC 80
GCGGACCCCGAAAGCTCTGACAGCGGGTGCAGTCTGGGCT 120
GGCGTCTCGCGTACCTTGGCCCCGGGAGCAGCGGACACACAC 160
CTTCCTCATCCACGGCGGGCAGCGCTTTAGCTAGCGGGAG 200
GCTGAGCGGGACAGCAACCGGATTCCTCGGCGCTTTCTGC 240
GGCGACCGGGCTGCGACCGGGGGCGCGCGAGGCTCGGGCAG 280
GGCGAGCACTGACCAAGGCGCAGCGGTGGCGGCTCGGGCT 320
GGAGATCGGGCTGCTAGAGCGACCAACCGGCCCCCTCTGG 360
CACCCTGGGGGACCGGTGGCGCTGCTCTCCCTAGCGGGCCC 400

Figure 8A

09405504-092309

GGATTTCCTTTGGATTHTGGTTGGACTGGCCAAAGCTGGC 440
CTGGGCAAGGCGCTTTGTGCGCACCGCTTTACGGCGAGGAC 480
CCCTGCTGCACTGCGCTCGGAGCTGGGGTGGAGTGGCT 520
CGTGCTGGCCACAGAGTTCCTGCGAGTCCCTGGAGCGGAC 560
CTGCGCGGCTTTCAGAGCCATGGGGCTCCACCTATGGGCGA 600
CGGGCGCTGAACTAATGTAGCTGGAATCAGCAATTTGCT 640
ATCGGAAGCAGCAGACCAAGTGGATGAGCCAGTGGCGGG 680
TACCTCTCTGCGCGCGCACATAATGCAACCTGCGCTGT 720
ACATCTTCACTCTGCGCACTACTGGCGCTGCGCAAGGCTGC 760
TCGATATCAGTATCTGAGGTTCTACAGTGGCAGGATTC 800
TAACATCTGTGTGGAGTCCAGCAGGAGGAGTCTTACC 840
TOGCACTCGGCACTGTACCATGTCTGGCTCCCTTCTGGG 880
CATTTGTGGGGTCTTGGGCTTGGGGCGACCGTGGTCTG 920
AAACCCAGTTCCTAGCTAGCGAGTCTTGGGAGGATTC 960
AGAAACACAGGGTGCAGTGTTCAGTACATTTGGGAGTT 1000
GTGCGGATACCTGCTCAACCGAGCGCGGAGGAGGAG 1040
TTTGACCATAGGTTGGGCTTGGGAGTGGGAGTGGGTTGC 1080
GCGCAGACACCTGGGAGCGTTTCCTGGGGGATTTGGACC 1120
TCTGCAGATACTGGAGAGGTATGGCATGACAGAGGGCAAC 1160
GTAGCTACGTTCAATTACACAGGAGCGGAGGGTGCAGTGG 1200
GGCGAGCTTCCTGGCTTTTACAGCAATCTTCGCTTCTC 1240
CTTGATTGATACGATGTGATGACAGGGGAGCGCTATTGG 1280
AATGCGGAGGGGCACTGCATGACACATCTCCAGGTGAGC 1320
CAGGCGTACTGGTGGCGCGAGTGGGAGGAGTCCCGCTT 1360
CCTGGGCTATGCTGGGGCTCCGGAGCTGGGCAAGGACAAG 1400
CTGCTCAAGGATGTCTTCTGGTCTGGGGAGGTTTCTTCA 1440
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TCACITOCAGATGCTGCTGAGACACCATCAGGTGGAAG 1520
GGAGAGAATGTGGCCCAACTGAGGTGCGTGGTCTTGG 1560
AGACCGTGGACTTCCTTCAGGAGGTGAACATCTATGAGT 1600
CAOGGTGGCAGGGCAAGAGGAGGGGAGGCAATGGGGCC 1640
TTGGCTCTGGCGCGCGCGGAGGCTCTGAACCTGGTGCAGC 1680
TCTACAGGCATGTTTCTGAGAACTTGGCAOOGTATGCGCG 1720
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GACACCTTCAACAGCAGAGGTTAGGATGGGCAATGAGG 1800
GCTTTTCAACCGAGTGTACTGTCTGACCCACTCTATGTTCT 1840
GGACCAAGATATAGGGGCTACCTGCGCGCTCACACCTGCC 1880
CGGTACAGTGGCGCTCTGTCTGGAGACCTTCTGAATCTGAA 1920
ACCTTCCACTTTCAGGAGGGGCTCGGAGGTTACAGGCGAC 1960
CATGGCTGCACAGGAGGGGTTTTCGGGTATCTTTTGTAT 2000
ATGCAGTATTTTGTATTAATAACAGCTGAGCTTAAAA 2040
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2080
AAAAAA 2087

Figure 8B

immFATP3 protein sequence

AADPESSESGCSLAWRLAYLAREQPTHTFLIHGAQRFSYAEAFERESNRIA 50
 RAFLRARGWIGGRRGSGRGSTEEGARVAPPAGDAAARGITAPPLAPGATV 100
 ALLLPAGEPDFLWIWFLAKAGLRTAFVPTALRRGFLIHCLRSCGASALVL 150
 ATEFLESLEPDLPALRAMGLHLWATGPEINWAGISNLLSEAADQVDEFPV 200
 GYLSAPQNTMDTCLYLFISGTTGLPKAARISHLKVLCQGFYHLCGVHQE 250
 DVTYLAALPLYHMSGSLIGIVGCLGIGATVVLKPKFSASQFWDDCQKHRVI 300
 VFQYIGELCRYLMNQPPSKAEFDHKVRLAVGSGLRPDIWERFLRRFGELQ 350
 ILETYGMTEGNVATENYTGRCQAVGRASWLYKHIFPFSIRYDVMICEPT 400
 RNAQGHOMTTSPEFGLLVAPVSQOSPFLGYAGAPELAKDKLLKDVFWSG 450
 DVFENIGDLLVCDEQGFLLHFHRTGDTIRWKGENVATTEVAEVLEITLDFL 500
 QEVNLYGVIVPGHEGRAGMAALALRPPQALNLVQLYSHVSENLPYARPR 550
 FLRLQESLATTETFKQOKVRMANEGFDPSVLSDFLYVLDQDIGAYLPLTP 600
 ARYSALLSGDLRI 613

Figure 9

immFATP4 DNA sequence

CCCAAGCGTCCGCCCCAGCGTCCGGCATGGCCAAGCTGGG 40
 CGTGGAGCGCGCTCTCATCAACACCAACCTTAGCGGGAT 80
 GCGCTGCGCCACTGTCTTGACACCTCAAAGGCACGAGCTC 120
 TCATCTTTGGCAGTGACATGGCCTCAGCTATCTGTGAGAT 160
 CCATGCTAGCCTGGAGGCCACACTCAGCCTCTTCTGCTCT 200
 GGATCCTGGGAGGCCAGCAGTGCCCGTACGACACAGAGC 240
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 CAGTCACCCAGACAAGGGTTTACAGATAAGCTCTCTTAC 320
 ATCTACACATCGGGCACCACGGGGCTACCCAAAGCTGCCA 360
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 GTACTATGGATTCCGCATCGGGCTGATGACATTGTCTAT 440
 GACTGCCCTCCCGCTCTACCACTCAAGCAGGAACATCGTG 480
 GCGATTGGCAGTGCTTACTCCACGGCATGACTGTGGTGAT 520
 CCGGAAGAAGTTCTCAGCCTCCCGGTTCTGGGATGATTGT 560
 ATCAAGTACAACCTGCACAGTGGTACAGTACATTGGCGAGC 600
 TCTGCGGCTACCTCCTGAACACAGCCACCCCGTGAGGCTGA 640
 GTCTCGGCACAAGGTGCGCATGGCACTGGGCAACGGTCTC 680
 CGGCAGTCCATCTGGACCGACTTCTCCAGCGGTTCCACA 720

Figure 10A

09405504 1052396

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CTGTAGCCTGGGCAACTTTTACAGCGGGGTGGGGGCTGT 800
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GGGACCCCGATGGAGTCTGCAATTCCTGTCAACCAGGTGAG 920
CCAGGCCAGCTGGTGGGTGGCATCATCCAGCAGGACCCCTC 960
TGGCGCGTTTCCAGCGGGTACCTCAACCAGGGTGGCAACAA 1000
CAAGAAGATTGTCTAATGATGTCTTCAAGAAGGGGGACCAA 1040
GCTTACCTCACTGGTTCAGTCCCTGGTTCATGATGAGCTGG 1080
GTTAOCCTGTACTTCCGACATGGCACTGGGGACACGTTCCG 1120
CTGGAAGGGGGAGAATGTATCTTACCACTGAGGTGGAGGGC 1160
ACACTCAGCGCGCTGCTTCATATGGCAGATGTGGCAGTTT 1200
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TCTGTCTCTTCCCTGGCTGTCTGTGAGTCTGTGTGTCTCT 2160
CATCTGTCTTACCTGAGTGTGGGTGGCAACAGGCATGAGG 2200
AGAGTGTGGCTCAGGGGGCAATAAATCTGCTTGTACTCC 2240
TCTTAAAAA 2280
AAAAA 2301

Figure 10B

mmFATP4 protein sequence

HASAHASGMAKLGVEAALININLRRDALRHCLDISKARAL 40
 IFGSEMASAICEITHASLEPILSLFCSGSWEPSIVFVSTEH 80
 LDPLLEDAPKHLPSHPDKGFTDKLFYTYTSGITIGLEKAAI 120
 VHSRYRMAASLVYYCFRMRPDDIVYDCLFLYHSSRKHRG 160
 DWQCLIHGMIVVIRKKEFSASREWDDCIKYNCTVVOYIGEL 200
 CRYLLNQPPREAFESRHKVRMALGNGLRQSTWIDFSSRFHI 240
 PQVAEFYGATECNCSLGNFDSRVGACGENSRILSFVYPIR 280
 LVRVNEDIMELIRGPDGVCTPCQPGQPGQIVGRTIQQDPL 320
 RRFDGYLNQGANNKIANDVEKKGDQAYLITGNLVMDELG 360
 YLYFRDRITGDI FRWKGENVSTIEVEGILSRLLHMAVAVY 400
 GVEVPGTEGRAGMAAVASPI SNCDLESFAQILKKELEPLA 440
 RPIFLRFLPELHKITGTFKFQKTEL RKEGFDPSVVKDPLFY 480
 LDARKGCYVALDQFAVIRIQAGEEKL 507

Figure 11

mmFATP5 DNA sequence

CACTCATCAGAGCTAAGAGAGACTACAGGCTCTCATCTAC 40
 TTCAGAAAGAGCCAAATGCCATGGGATTTTGGAGAAACTA 80
 ACCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 AGCCCCCATGCGCAGCAGCTATGGCTCTGCGCCCTGCGGTG 160
 GTTCCTGGGAGACCCACATGCGCTGCTGCTGCTGCTGCTG 200
 GCATTGCTGGGCGAGACCGTGGATCAGCTCCTGGATGCCCC 240
 ACTGGCTGAGCGCTGGTAGGAGCAGCTCTTAACCTTATTCCT 280
 ATTGCTCTTACAGCCACCCCCAGGGCTAGCGCTGGCTGCAT 320
 AAAGATGTTGGCTTTCAACCTTCAAGATGCTTTTCTATGGCC 360
 TAAAGTTTCAAGGCGAGCGCTTAAACAAACATCCTCCAGAGAC 400
 CTTTGTGGATGCTTTAGAGCGGCAAGCACTGGCATGGCCT 440
 GACCGGGTGGCGCTGGTGTGTTACTGGGCTCTGAGGGCTCCT 480
 CAATCACAATAAGCCAGCTGGATGCCAGGTCCTGTACAGGC 520
 AGCATGGGCTCCTGAAAGCAAAGCTGAAGGATGCCGTAATC 560
 CACAACACAAGAGATGCTGCTGCTATCTTAGTTTCTCCCGT 600
 CCAAGACCATTTCTGCTTTTGTAGTGTGTTTCTGGGGTTGGC 640
 CAAGTTGGGCTGCCCTGTGGCTGGATCAATCCACACAGC 680
 CGAGGGATGCCCTTGGCTACACTCTGTACGGAGCTCTGGGG 720
 CCAGTGTGCTGATTGTGGATCCAGACCTCCAGGAGAACCT 760
 GGAAGAAGTCCCTTCCCAAGCTGCTAGCTGAGAACATTAC 800

Figure 12A

04105504 092399
 155250 "H0550460

562250" 40550460

TGCTTCTACCTTGGCCACAGCTCACCCACCCCGGGAGTAG 840
AGGCTCTGGGAGCTTCCCTGGATGCTGGCAGCTTCTGACCC 880
AGTACCTGGCAGCCTTCGAGCTACGATTAAAGTGGAAATCT 920
CCTGGCCATATTTCATCTTTACTTTCAGGGACCACTGGACTCC 960
CAAAGCCAGCCATCTTTATCAGATGAGGGGGTCATACAAGT 1000
GAGCAACCTGCTGTCCCTTCTGTGGATGCGAGAGCTGATGAT 1040
GTGGTCTATGAGCTCCCTACCTCTGTACCATACGATAGGGC 1080
TTGTCCCTTGGATTCCCTTGGCTGCTTACAAGTTGGAGCCAC 1120
CTGTGTCTCTGGCCCCAAGTTCTCTGCTCCCTCCGATTCTGG 1160
GCTGAGTCCCGCCAGCATGGGTAAACAGTATCTTTGTATG 1200
TGGGTGAAATCTCTGGGTAAGTTGTGTAAAGTCCCTGAGCA 1240
ACGAGAAGACAAGATACATACAGTGGCTTGGCCATGGCA 1280
ACTGGACTTCCGGCAAAATGTGTGGCAAAAACCTCCAGCAAC 1320
GCTTTGGTCCCATTCGGATCTGGCAATTCTACGGATCCAC 1360
ACAGGGCAATGTGGGCTTAATGAACATATGTGGGCCACTGC 1400
GCGGCTGTGGGAAGGACAGCTGCATCCCTCGAATGCTGA 1440
CTCCCTTTTGAAGCTTGTACAGTTCCACATAGACAGCAGA 1480
GCTCTGTAGGGACAAACAGGGTTTTTTCATTCTGTGGAG 1520
CCAGCAAGCCAGGACTTCTTTTGAACCAAGGTTCCGAAAGA 1560
ACCAACCCCTCTCTGGGCTACCGTGGTTCCAGGCCGAGTC 1600
CAATCGCAAACTTGTGTGGCAATGTACCAAGGTTAGGAGAC 1640
CTGTACTTCAACACTGGGGAAGGTGCTGAACCTTGGACCCAG 1680
AAGGCTTCTCTTACTTTTCAAGACCCGCTTGGTGACACCTT 1720
CCGGTGGAAAGGCGAAACGGTATCTACCTGAGAGGTTGGAG 1760
TGTTGTTTTGTCTAGCTTACCTTCTACCTGAGGAGTCAATG 1800
TCTATGGTGTGCTGCTGCTCCAGGGTGTGAGGGTAAGGTTGG 1840
CATGGCTGCTGTGAAACTGGCTCCCTGGCAAGACTTTTGAT 1880
GGGCAGAAAGCTATACAGCATGTCCGCTCCCTGGCTCCCTG 1920
CCATATGCCACACCTCATTTTCATCCGTATCCAGGATTCCCT 1960
GGAGATCACAACACCTTACAAGCTGGTAAAGTACGGCTTG 2000
GTGGGTGAGGGTTTTGATGTGGGGATCATTGCTGACCCCC 2040
TCTACATACCTGGACAACAAGGCCACACCTTCCGGAGTCT 2080
GATGCCAGATGTGTACCAAGGCTGTGTGTGTAAGGAACCTGG 2120
AATCTCTGACCAACCTAGCCAACTGGAAGGCAATCCAAAAG 2160
TGTAGAGATTGACACTAGTACGCTTACAAAGTTGTCCGG 2200
GTTCCAGATGCCCATGGCCAGTAGTACTTAGACAATAAA 2240
CTTGAATGTGTATACAAAAA 2277

Figure 12B

mmFATP5 protein sequence

MALALFWFLGDPTCLNLLGLALLGRFWLSSWMPHWSLVG 40
 AALTLFLLPLQPPFGLRWLHKDVAFTFKMLFYGLKERRRL 80
 NKHPPEIFVDALERQALAWPDRVALVCTGSEGSSTINSQL 120
 DARSCQAAWLKAALKDAVIQNIRDAAATLVLPSKTTISAL 160
 SVFLGLAKLGCFVAWINPHSRGMPLIHSVRSSGASVLIVD 200
 PDLQENLEEVLPKLLAENIHCFYLGHSSPTFGVEALCASL 240
 DAAPSDFVPASLRATIKWKSPATFIFTSGTTGLPKPAILLS 280
 HERVIQVSNVLSFCGCRADDVYDVLPLYHTTGLVLGFLG 320
 CLQVGATCVLAPKFSASRFWAECRQHGVIIVILYVGEILRY 360
 LCNWPEQPEDKTIHVRLAMGTGLRANWKNFQORFGPIRI 400
 WEFYGSTEGNVGLMNYVGHOGAVGRTSCILRLITPPELVQ 440
 FDIETAEPLRDKQGFCLFVEFGKPGILLIKVRKNQPFLLGY 480
 RGSQAESNRKLVANVRRVGDLYFNIGLVLITDQEGFFYFQ 520
 DRLGDIFRWKGENVSTIGEVECVLSSLDLEEVNVYGVFVP 560
 GCEGKVGMAAVKLAPGKTFDQKLYQHVRSWLPAYATEHF 600
 IRIQDSLEITNTYKLVKSRLVREGFDVGLIADPLYILINK 640
 AQTFRSLMPDVYQAVCEGIWNL 663

Figure 13

hsFATP2 DNA sequence

ATGGGATTGACTCCTTCTGACAAAGTGGATGAAGTATC 40
 AACTGAACCTATCCCAGAGTCATGGAGGCTGAAGTCACT 80
 TTTTCCACTCCTGCCCTATACATTTATACCTTCGGAACCA 120
 CAGGCTCTCCAAAAGCAGCCATGATCACTCATCAGCGCAT 160
 ATGGTATGGAAGTGGCTCACTTTTGTAGCGGATTGAAG 200
 GCAGATGATGICATCTATATCACTCTGCCCTTTTACCACA 240
 GTGCTGCACTACTGATTGGCAATTCACGGATGATTTGIGGC 280
 TGGTGCTACTCTTGCCCTTGCGGACTAAATTTTCAGCCAGC 320
 CAGTTTGGGATGACTGCAGAAAATACAAAGTCACTGTCA 360
 TTCAGTATATCGGTCGAACCTGCTTCGGTATTTATGCAACTC 400
 ACCACAGAAACCAATGACCGTGATCATAAAGTGAGACTG 440
 GCACCTGGGAAATGGCTTAACGAGGAGATGTGTGGAGACAAT 480
 TTGTCAAGAGATTTTGGGGACATATGCATCTATGAGTTCTA 520
 TGCTGCCACTGAAGGCAATATTGGATTATGAATTATGCG 560
 AGAAAAGTTGGTGCCTGTTGGAAGAGTAAACTACCTACAGA 600
 AAAAAATCATAACTTATGACCTGATTAAATATGATGTGCA 640
 GAAAGATGAACCTGTCCGTCATGAAAATGCATATTGCGTC 680
 AGAGTTCCCAAAGGTGAAGTTGCACTTCIGGTTTGCAAAA 720
 TCACACAACCTACACCATTTAATGGCTATGCTGGAGCAA 760
 GGCTCAGACAGAGAAGCAAAAACCTGACAGATGCTTTAAG 800

Figure 14A

ACACCTTCAGGTGCAAGGGGAGCAATGTGGCCACAACCGA 200
 GGTGGCAGAGGTCTCTGAGGGCCCTAGATTTTCTTCAGGAG 240
 GTGAAGGCTCTATGCGAGTCACTGTGCCAGGGCATGAAGGCA 280
 GGGCTGGAATGGCAGCCCTAGTTCTGTGGGTCCCCCCCCACGC 320
 TTTGGACCTTATGCGAGCTCTACACCCAGGTGTCTGAGAAC 360
 TTGCCACCTTATGCCCCGGCCCCGATTCTCAGGCTCCAGG 400
 AGTCTTTTGGCCACCACAGAGACCTTCAAAACAGCAGAAAGT 440
 TCGGATGGCAAATGAGGGCTTGAACCCAGCACCCTGTCT 480
 GACCCACTGTAGGTTCTGCAACAGGCTGTAGGTGCTTACC 520
 TGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCTGCGCAGG 560
 AAACCTTTCGAATCTGAGCAACTTCCACACCTGAGGCAOCTG 600
 AGAGAGGAACCTCTGTGGGGGGGGGGGGGGGGTGCAGGIGTAC 640
 TGGGCTGTGAGGGATCTTTTCTATACCAGAACTGGGGTCA 680
 CTATTTTGTAAATAAATGTGGCTGGAGCTGATCCAGCTGIC 720
 TCTGACCTACAAAAA 753

Figure 16B

hsFATP3 protein sequence

QFGTFRGIVWPHLQVSQKLLKDVFRPGDVFFNIGDLLVC 40
 DDQGFLEFRHDFRIGDIFRWKGENVATTEVAEVFEALDFLQE 80
 VNVYGVIVPFGHEGRAGMAALVLRPPHALDLMOLYTHVSEN 120
 LPPYARPRFLRLQESLATTETFKQKVRMANEGFDPSILS 160
 DPLYVLDQAVGAYLPLTTARYSALLAGNLRI 191

Figure 17

hsFATP4 DNA sequence

TCAAGTACAACCTGCACGATTGTGCATANCATTGGTGAACCTG 40
 TGCCGENTACCTCTGTAACAGCCACCGCGGGAGGCAGAAA 80
 ACCAGCACCAGGTTTCGCATGGCACTAGGCAATGGGCTCCG 120
 GCAGTCCATCTGGACCAACTTTTCCAGCCGCTTCCACATA 160
 CCCCAGGTGGCTGAGTTTACGGGGCCACAGAGTGCACACT 200
 GTAGCCTGGGCAACTTGCACAGCCAGGTGGGGGCTGTGG 240
 TTTCAATAGCCGCACTCTGTCTTGTGTGTAACCCATCCGG 280
 TTGGTACGGTGTCAACAGGACACCATGGAGCTGATCCGGG 320
 GGGCGGACGGGGTCTGCAATTCCTGCCAGCCAGGTGAGCC 360
 GGGCCAGCTGGTGGGGCCATCATCCAGAAAGACCCCTG 400
 CGCGCTTTCATGGCTACCTCAACAGGGGGCCACACA 440
 AGAAGATTGCCAAGCATGTCTTCAAGAGGGGGACAGGC 480
 CTACCTTACTGGTGATGTGGCTGGTGATGCACAGCTGGCC 520

Figure 18A

09405504-1092390

TACCTGTAAGTTCCTGACCGCACTGGGCAACAGTTCCGCT 560
 CGAAAGGTGAGAACGGTGTCCACCAACGAGGTGGAAGGCAC 600
 ACTCAGCGCGCTGCTGACATGGCTGACGTGGCGGTGTAT 640
 GGTGTGCGAGGTGCCAGGAACCGAGGGCGGGCGCGGAATCG 680
 CTGCTGTGGCGACCGCACTGGCAACTGTGACCTGGGAGC 720
 GCTTCTGCTCAGGTC 734

Figure 18B

hsFATP4 protein sequence

IGELCRYLLNQPPREAFNQHVRLMALGNLRQSIWINESS 40
 RFHIPQVAEFYCATENCSLGNFDSQVACGFNSRILSFV 80
 YPIRLVVRNEDIMELIRGPDGVCIPQPGEPQIVGRILQ 120
 KDPLRRFDGYLNDGANNKKIAKLVFKKEDQAYLITGDVLM 160
 DELGYLYFRDRITGDIKRWKGENVSTTEVEGILSRLLIMAD 200
 VAVYGVVEVPGIEG 213

Figure 19

hsFATP5 DNA sequence

CNIGCCCTCTGTACCAACGGTATGGCACTTTGTGCTTGGCA 40
 TCCTGGCTGCTTACATCTCGGAGCCACCTGTGTCTGGC 80
 CCCCCAGTTCCTACTTCTGCTTCTGGCATGACTGTGG 120
 CAGCATGGCGTGACAGTGATCTGTATGTGGCGAGCTTC 160
 TGCTACTTGTGTACATTCCTCCAGCAACAGAGGACCG 200
 GACACATACAGTCCGCTGGCAATGGSCAATGCACTACGG 240
 GCTGATGTGTGGGGGACCTTCCAGCAGCGTTTGGGTCT 280
 ATTTCCGATCTNGGCAAGTCTTACGGGCTTCCACAGAAG 320
 GCAACATGGGGCTTTAGTTCACCTATTTGTGGGGGGCTG 360
 CCGGGGSCCTGCGGGCAAGATGGAGCTTGGCTCTCCGAA 400
 TGCTGTCCCCCTTTGAGCTGGTGCAGTTGCATGCGAGG 440
 GGCGGAGCTGTGAGGGACAATCAGGGCTTCTGCATCCCT 480
 GTAGGGCTAGGGGACCGGGGCTGCTGTGACCAAGGTGG 520
 TAAGCCAGCAACCTTCTGTTGGGCTACCGCGGGCGGCGA 560
 GCTGTGGCAACGCAAGCTGGTGGCAACGTGGGCAATCG 600
 GCGCAAGTTTACTACAACACCGGGGACGTACTGGCATGG 640
 ACCGGCAAGGCTTCTCTACTTCCGCAACGACTCGGGGA 680
 CACCTTCCGATGGAAGGGGAGAACGTGTCCAGCAACAG 720
 GTGCAAGGCGGTGTGTGGCAGGTGGACTTCTTGCAACAG 760
 TTAACGTGTATGGCGGTGTGGTGGCAGGTGTGAGGGTAA 800
 GGTGGGCATGGCTGCTGTGGCATTAGCCCCGGGCACT 840

Figure 20A

09405504-092390

Figure 20B

Figure 21

Figure 21

Figure 21

Figure 22A

AATGGCTTCTATTATTTTAAAAACCAATACATCTTTAGAT 760
 TTGCAAAAAGTTTATGAACAAGTTGTAACATTTCTACCAG 800
 CTTATGCTTGTCCACGATTTTAAACAATTCAGGAAAAAAT 840
 GGAAGCAACAGGAACATTCAAACTATTGAAGCATCAGTTG 880
 GTGGAAGATGCATTTAATCCACTGAAAATTTCTGAACCAC 920
 TTTACTTCATGCATAACTTGAAAAAGTCTTATGTTCTACT 960
 GACCAGGGAACITTTATGATCAAATAATGTTAGGGGAAATA 1000
 AAACITTTAAGATTTTATATCTAGAACTTTTCATATGCCTT 1040
 CTTAGGAACAGTGCAGAGGGGGTATATGATTCCTTTATGAA 1080
 ATGGGGAAGGGAGCTAACATTAATTATGCATGTACTATA 1120
 TTTCCTTAATATGACAGATAATTTTTTAAATTGCATAAGAA 1160
 TTTTAATTTCTTTTAAATTGATATAAACACAGTTGATTATT 1200
 CTTTTTATCTATTITGAGATTTCAGTGCATAACTAAGTATT 1240
 TTCCCTTAATACTAAAGATTTTAAATAATAAATAGTGGCTA 1280
 GCGGTTTGGACAATCACTAAAAATGTACTTTCTAATAAGT 1320
 AAAATTTCTAATTTTGAATAAAAGATTAAATTTTACTGAA 1360
 A 1361

Figure 22B

hsFATP6 protein sequence

ACVLKKKFSASQFWSDCRKYDVIVFQYIGELCRYLCKQSKREGEKDHKVR 50
 LAINGIRSDWREFLDREFGNIKVCELYAATESSTSEFMNYTGRIGAIGRT 100
 NLFYKLLSTFDLKYDFQKDERMRNEQGWFMKRKRRPGLLISRVNAKNPF 150
 FGYAGPYKHKKDKLLCDVFKKGVYLNIGDLIVQDQINFLYFWRIGDIF 200
 RWKGENVATTEVADVIGMLDFTQEFANVYGVALSQYECRAGMASIILKENT 250
 SLDLKQVYEQVIFLPAYACPRFLRIQEKMEATGIFKLLKHQLVEDGFNP 300
 LKISEPLYFMDNLKKSIVLLITRELYDQIMLGEIKL 335

Figure 23

mtFATP DNA sequence

TAGTCGATAACGTCAAGGACGCTCTGCGGGGCTGCGCACC 40
 TTGCTGAGGTTGGTGACAACCAATTCACATTTGCGAAA 80
 CGAATCGAGGGCTTACGTTGTCCGATTACTACGGGGGGGCA 120
 CACACAACGGTCAGGCTGATCGACCTGGCAACTCGGATGC 160
 CGCGAGTGTGTGGCGCACACGCGGGTCAATTGTGCGTGGGGC 200
 AATGACCGGGCTGCTGGGCGGGCGGAATTCCAAGGCGTGC 240
 ATCGGCACGGTGTTCAGGACCGGGCGGGCTGCGTACGGTG 280
 ACCGAGTCTTTCCTGAATTCGGCGATCAGCAGCTGACCTA 320
 CCGCGACGCTAACGCCACCGCCAACCGGTACGGCGGGTG 360

Figure 24A

TTCGGCGCCGCGGGGTTCGGCCCCGGCGACGTTCGTTCGCCA 400
TCTATGTTCGGTAACCTCACCCAGCAGCTCTTGCGCATGCT 440
GGCCACGGTCAAGTGGGGGCTATCGCCGGCATGCTCAAC 480
TACCACACAGCGGGGGAGGTTGTTGGCGCACAGCTGGGTC 520
TGCTCGAACGGGAAGTACTGATCGCACAGTCCGACTTGGT 560
CAGCGCGGTTCGGCAATGCGGGGGCTTCGGCGGGCGGGTA 600
GCGGGCGACGTCTGACCGTTCGACGACGTTGCAGGATTTCG 640
CCACAACGGCGCGCCGCCAACAAACCGGGGTTCGGCGTTCGGC 680
GGTGCACAGCCAAGAACAACCGGGTTCTACATCTTTCACCTCG 720
GGCACACACGGGATTTTCCCAGGCGAGTGTTCATCAGGCTATC 760
ATCGGTGGGTTCGGGGGGCTGGCGGTCTTTCGAGGGATTCGG 800
GCTGCGGCTGAAGGGTTCCGACACGGCTCTACAGCTGCTG 840
CCGCTGTACCAACAACAACGGGTTAACGGTTCGGGGTGTCTGT 880
CGGTGATCAATTCTGGGGGACCGCTGGCGCTGGGTAAAGTC 920
GTTTTTCGGGTTCGGGGTCTGGGATGAGGTGATTGCGAAC 960
CGGGCGACGGCGTTTCTTACATCGGCGAAATCTGCGGTT 1000
ATCTGCTCAACCAGCGCGCAAAGCGCACCGACCGTTCGCA 1040
CCAGGTTCGGGGTGATCTGCGGTAAACGGCTTCGGCGGGAG 1080
ATCTGGGATGAGTTCAACACCGCTTCGGGGTTCGGCGGG 1120
TGTCGAGTTCTACCGCGCCAGCGAAGGCAACTCGGCTT 1160
TATCAACATCTTCAACGTGCCCCAGGACCGCGGGGTATCG 1200
CCGATGCGGCTTCGCTTTTGTGGAATAACCACTGGACACCG 1240
GGGATTCGCTTCGGGATTCGCGAGCGGGCGAGTTCGTTGGGT 1280
ACCCGACGGTGAACCCGGGCTGTTCCTTAGCGGGTCAAC 1320
CGGCTGCAGCGGTTTCAGCGCTACACCGACCCGGTTGCCA 1360
GGCAAAAGAGTTGGTTCGCAACCGCTTTTCAGATGGCGA 1400
CTGTTGGTTCAACACCGGTCAAGTATGAGCGCGCAGGGC 1440
ATGGGCCATGCGGCTTTCGTCATCGGCTTCGGCGACACT 1480
TTCGCTGCAAGGGCGACAAATGTTCGCAACACTCAGGTTCG 1520
AGCGGCACCTGGGCTTCGACCAACCGGTTCAGGAGTTCACG 1560
GTCTACGGCGTTCAGATTTCGCGCACCGCGGGCGGGCGCG 1600
GAATGGCGCGCATCAACTTCGCGGCTTCGGCGCGCAATTTCG 1640
CGGCGAGGCGCTTCGCGCAACGGTTTACGGTCACTTTCGCC 1680
GGCTATGCACTTTCGCTCTTTGTTTCGGGTAGTTCGGGTTCG 1720
TGGCGCACACCAACGAGTTCAAGAGTTCGCAAGGTTCGAGTT 1760
GCGCAACACAGGCTTATGGCGCGACATCGAGGATTCGCTG 1800
TACGTACTGCGCGCGCGCGCAAGGATATGTTCGCGTACT 1840
ACCGCGAATACCTTCAGGAGGTTTCGCTTCGCAAGCGGACC 1880
GCAGGGCTAGCGGATTCGCGGGCGAGTCTTCGATAACCGCA 1920
CTGGACGCTTCAGGTTAACAGGCACTATGATGCGGTTCG 1960
TTCAACACCGCGCGGCTCAGCGGTTCTTCAACACCGCGC 2000

GCGTTAG 2007

Figure 24B

mtFATP protein sequence

msdyyggahttvrlidlatmprvladtpvivrgamtgll 40
 arpnskasigtvfgdraarygdrvflkfgdqltyrdana 80
 tanryaavlaargvpgdvvgimlmspstvlamlatvkc 120
 gaiagnlryhgrgevlahslglldakvliaesdlvsavae 160
 cgasrgrvagdvltvedverfattapatnpasasavqakd 200
 tafyiftsgttgfpkasvmthhrwlralavfggmglrlkg 240
 sdtlyscplyhnmaltvavssvinsgatllalgksfsasr 280
 fwdevianratafvyigeicryllnqpakptdrahqvrvi 320
 cnglrlpeiwdettrfgrvarvcefyasegnsafinifn 360
 vprtagvspmplafveydlldtgdlrdasgrvrrvpdgep 400
 glllsrvnrllqpfdgytdpvasekklvinafrdgdwfn 440
 gdmvmpgmgghaafvdrldgtfrwkgenvattqveaalas 480
 dotveectvygvqiprtggragmaaitlragaeftggala 520
 rtvyghlpgyalplfvrvgslahtttfksrkvelmqay 560
 gadiedplyvlagpdegypyyaeypeevslgrmpcg 597

Figure 25

65E260:10550460

09405504 1092399

hsFATP1

1 tcy acc cac ggc gtc cgg gac ccc aaa gca gaa gcc cgc aca gta ggc aca gcy cac cca
61 aga agy gtc cag gag tct gca gaa aca gaa agy tcc ccy gcc tca gcc tcc tag tcc cty
121 cct gcc tcc tgc cty agc ttc cgg gag act gaa ggc acy gct tgc agc ttc agy acy cgg
M R
181 gcc ccy ggt gcy ggc gcy gcc tcy gty gtc tcy cty gcy cty tgy tgy cty gcy gcy cty
A P G A G A A S V V S L A L L W L L G L
241 ccy tgy acc tgy agc cgy gca gcy gcy cty gcc gty tac gty gcy agc gcy gcy cgy cgy
P W T W S A A A A L G V Y V G S G G W R
301 ttc cty cgc atc gtc tgc aag acc gcy agy cga gac ctc ttc ggt ctc tct gty cty atc
F L R I V C K T A R R D L F G L S V L I
361 cgc gty cgy cty gcy gcy cgy gcy ccy gcy ccy ccy gcy ccy ccy gcy ccy ccy gcy ccy
R V R L E L R R H Q R A G H T I P R I F
421 cag gcy gta gty cgy cga cag ccc gcy cgy cty gcy cty gty gat gcc ggy acc gcy gcy
Q A V V Q R Q P E R L A L V D A G T G E
481 tgc tgc acc ttc gcy cgy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
C W T F A Q L D A Y S N A V A M L F R Q
541 cty gcy ttc gcy cgy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
L G F A P G D V V A I F L E G R P E F V
601 ggy cty cgy cty gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
G L W L G L A K A G M E A A L L N V N L
661 cgy cgy gcy ccy cty gcc ttc tgc cty gcy acc tcy gcy gcy agy gcc cty acc ttc gga
R E P L A F C L G T S G A K A L I F G
721 gga gaa atg gty gcy gcy gty gcc gaa gty agc ggy cat cty ggy aaa agt tgy atc aag
G E M V A A V A E V S G H L G K S L I K
781 ttc tgc tct gga gac tgy ggy ccy gcy gcy atc tgy cgy gac acc ctc cty gcy cgy
P C S G D L G P E G I L P D T H L L D P
841 cty cty aag gcy gcy tct act gcc ccc tgy gca cag atc ccc agc aag gcy atg gac gac
L L K E A S T A P L A Q I P S K G M D D
901 cgt ctt ttc ttc atc ttc acy tcy ggy acc acc ggy cty ccc aag gcy gcc att gcy gty
R L F Y I Y T S G T T G L P K A A I V V
961 cac agc agy ttc ttc cgy atg gca gcc ttc gcy ccy ccy gcy ccy gcy ccy gcy ccy gcy
H S R Y Y R M A A F G H H A Y R M Q A A
1021 gac gcy cty ttc ttc cgy cty ccy cty ttc ccy gcy gcy gcy gcy gcy gcy gcy gcy gcy
D V L Y D C L P L Y H S A G N I I G V G
1081 cgy tgc ttc atc ttc ggy cty aca gty gty cty ccy gcy aag aaa ttc cgy gcc agc cgy ttc
Q C L I Y G L T V V L R K K F S A S R F
1141 tgy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
W D D C I K Y N C T V V Q Y I G E I C R
1201 ttc cty cty aag cgy cgy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
Y L L K Q P V R E A E R R H R V R L A V
1261 ggy aac ggy cgy cgt cct gcc atc cgy gcy gcy ttc acy gcy cgy ttc gcy gta cgy caa
G N G L R P A I W E E F T E R F G V R Q
1321 atc ggy gcy ttc ttc gcy gcc acc gcy tgc aac tgc agc att gcc aac atg gcy gcy aag
I G E F Y G A T E C N C S I A N M D G K
1381 gcy gcy ttc tgc ggt ttc aac agc cgy atc cty ccy ccy gcy ttc ccy atc cgy cty gty
V G S C G F N S R I L P H V Y P I R L V
1441 aag gcy aat gcy gcy aca atg gcy cty cty cgy gcy gcc cgy gcy ccy tgc atc ccy tgc
K V H E D T M E L L R D A Q G L C I P C
1501 cgy gcy gcy gcy ccy gcy cty cty gty gty cgy atc aac caa cgy gcy cgy cty gcy cgy
Q A G E P G L L V G Q I N Q Q D P L R R
1561 ttc gcy gcy ttc gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
F D G Y V S E S A T S K K I A H S V F S
1621 aag gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
K G D S A Y L S G D V L V M D E L G Y M
1681 ttc ttc cgy gcy cgy agc ggy gcy acc ttc cgy tgy cgy ggy gcy aac gty ttc acc acc
Y F R D R S G D T F R W R G E N V S T T
1741 gcy gty gcy gcy gty cty gcy cty cty gcy cgy aca gcy gty gcy gty ttc gty gty
E V E G V L S R L L G Q T D V A V Y G V
1801 gcy gcy ccy gcy gty gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy gcy
A V P G V E G K A G H A A V A D P H S L
1861 cty gcy ccy aac gcy ata ttc cgy gcy cgy aag gty cty gcy ccy ttc gcy gcy ccy
L D P N A I Y Q E L Q K V L A P Y A R P
1921 atc ttc cty cty cty ccy cgy gcy gcy acc aca gcy acc ttc aag atc cgy aag acy
I F L R L L P Q V D T T G T F K I Q K T
1981 agy cty cgy cgy gcy gcy ttc gcy ccy cgy acc tca gcy cgy cty ttc ttc cty gcy
R L Q R E G F D P R Q T S D R L F L D
2041 cty aag cgy gcy ccy ttc cty ccy ttc aat gcy gcy gcy ttc act cgy atc tgc tcy gcy
L K Q G H Y L P L N E A V Y T R I C S G
2101 gcy ttc gcy ccy tga agc tgc ttc ttc act gcy ccy aaa cty tgy gcc tgy tgy gcy agy
A F A L
2161 cca gcy tga gcc aga cgy cgy tgc cca ggy gcy gcc gcc tag tac aca ccy acc tgy cgy
2221 agc tgc acc tgy ccy ccy ccy ttc tgy act gcy aaa cty gaa ccy cgy agy aac cgy tgc
2281 ccy tcy gcy gcy ccy cty gcy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy
2341 ccy ttc atc ccy gcy ccy gcy ccy taa cty ttc ccy ccy ttc ccy ttc ccy ttc
2401 ttc ttc ttc aag ata gcy ttc ccy ttc gcy gcc cgy gcy aga gcy cgy tgy gcy gcy
2461 cty gcy tca cty caa ccy cty ccy ccy gcy gcy ccy ccy ccy ccy ccy ccy ccy ccy
2521 gcy tag cty ggy tta cgy gcy ccy gcc acc acy tcc agc taa ttc tta tat ttc tag tag
2581 aga cgy gcy ttc acc atg tcy gcy agy cty gcy tcy aac ccy tga ccy cgy gcy atc ccy
2641 tgy ccy cgy ccy ccy aga gty cty ggy tta tag cgy tga gcc tcy gcy ccy ttc ccy
2701 ttc ttc ttc ccy cty cty cgy aga gty gaa ccy acy tgc ccy ggy agc tgc atc tgy tgc
2761 agy gcy cgy cty cty tgy ggy acc gcy ggy acc ccy ccy ggy ccy tgy acc cgy acc
2821 ggy gcc ttc ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy
2881 gcy gty ggy ttc cgy atg cgy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy
2941 tgy tga atg gcy cgy ggy gty ccy ccy gcy aac cgy aaa atc tcc cgy gcy agy ccy
3001 act gcc ttc tgc act tcc cgy ttc cty tca cat ttc ccy agc ccy acc ttc ccy tcc tga
3061 tgc ccy gaa agc ttc cgy aat tga cty tga ccy ttc gga tgc ccy ccy tgc ccy ccy cty
3121 ccy gcy tgc ccy cat tta gcc atc tcc atg gcy cty cty gcy gcy ccy gcy ccy ccy
3181 act gcy tgy ccy ccy agc cgy cty ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy
3241 atc tgy tgc gcy ccy tgy agy gty ccy cgy gcy agy cgy cgy gcy ccy ccy gcy ccy
3301 ccy gcc ggy ggy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy ccy
3361 ggy ggy tgy ccy ccy cgy tgc ccy ccy tga tgy ccy tga ccy gcy gcy gcy gcy gcy
3421 ccy gcy aac ccy acc agy agy gcc cgy aca tcc cty cty gcy tcy cty gcy gcy ccy
3481 gaa cat ccy ccy ccy ttc tgy gcy cgy ccy acc agy ccy ccy gcy ccy ccy tcc tcc
3541 ccy cgy ccy ccy ccy gcy ccy gcy gcy ccy acc agy ccy ccy gcy ccy ccy tcc tcc
3601 ccy atg tga acc ttc cty gcy act gty gty tta ttc ccy aat tga ttc aag aca ccy cgy
3661 tga aga cgy ccy ggy gaa aaa aaa aaa aaa agy gcy gcc gc

hsFATP4

1 cga ccc acg cgt ccg ggc ggg cgg ggc cgg gcg gcg ggc ggg gct ggc ggg gcg gcc ggg
61 cca tgc agg ggc cag agc cgg cta aac cct gct gag acc cgg ctc cgt ggc tcc agg ggc
121 ggc taa tgc ccc tca cgc tgc cta cgc tgc tgc aac cgg gcc gca tct gga cgg ggc gcc
181 gcg cgg cgg agc cga cgc cgg gcc aca atg ctg ctt gga gcc tct ctg ggg ggg ctg
M L L G A S L V G V L
241 ctg ttc tcc aag ctg gtc ctg aaa ctg ccc tgg acc cag gtc gga ttc tcc ctg ttg ttc
L F S K L V L K L P W T Q V G F S L L P
301 ctc tac ctg gga tcc ggc ggc tgg cgc ttc atc cgg gtc ttc atc aag acc atc agg cgc
L Y L G S G G W R F I R V F I K T I R R
361 gat atc ttt ggc cgc ctg gtc ctc ctg aag gtc aag gca aag gtc cga cag tgc ctg cag
D I F / G G L V L L K V K A K V R Q C L Q
421 gag cgg cgg aca gtc ccc att ttg ttc gcc tct acc gtt cgg cgc cac ccc gac aag acg
E R R T V P I L P A S T V R R H P D K T
481 gcc ctg atc ttc gag ggc aca gat acc cac tgg acc ttc cgc cag ctg gat gag tac tca
A L I F E G T D T H W T F R Q L D E Y S
541 agc agt gta gcc aac ttc ctg cag gcc cgg ggc ctg gcc tgg ggc gat gtc gct gcc atc
S S V A N F L Q A R G L A S G D V A A I
601 ttc atg gag aac cgc aat gag ttc gtc ggc cta tgg ctg ggc atg gcc aag ctc ggt gtc
F M E N R N E F V G L W L G H A K L G V
661 gag gca gcc ctc atc aac acc aac cgc cgg cgg gat gct ctg ctc cac tgc ctc acc acc
E A A L I N T N L R R D A L L H C L T T
721 tgg cgc gca cgg gcc ctt gtc ttt ggc agc gaa atg gcc tca gcc atc tgt gag gtc cat
S R A L V F G S E M A S A I C E V H
781 gcc agc ctg gac ccc tgc ctc agc ctc ttc tgc tct ggc tcc tgg gag ccc ggt ggc gtc
A S L D P S L S L F C S G S W E P G A V
841 cct cca agc aca gaa cac ctg gac cct ctg ctg aaa gat gct ccc aag cac ctt ccc agt
P P S T E H L D P L L K D A P K H L P S
901 tgc cct gac aag ggc ttc aca gat aaa ctg ttc tac atc tac aca tcc ggc acc aca ggg
C P D K G F T D K L F Y I Y T S G T T G
961 ctg ccc aag gcc gcc atc gtc gtc cag agc agt tat tac cgc atg gct gcc ctg gtc tac
L P K A A I V V H S R Y Y R M A A L V Y
1021 tat gga ttc cgc atg cgg ccc aac gac atc gtc tat gac tgc ctc ccc ctc tac cac tca
Y G F R H R P N D I V Y D C L P L Y H S
1081 gca gga aac atc gtc gga atc ggc cag tgc ctg ctg cat ggc atg acg gtc gtc att cgg
A G N I V G I G Q C L L H G M T V V I R
1141 aag aag ttc tca gcc tcc cgg ttc tgg gac gat tgt atc aag tac aac tgc acg att gtc
K K F S A S R F W D D C I K Y N C T I V
1201 cag tac att ggt gaa ctg tgc cgc tac ctc ctg aac cag cca cgg cgg gag gca gaa aac
Q Y I G E L C R Y L L N Q P P R E A E N
1261 cag cac cag gtt cgc atg gca cta ggc aat ggc ctc cgg cag tcc atc tgg acc aac ttt
Q H Q V F M A L G N G L R Q S I W T A N P
1321 tcc agc cgc ttc cac ata ccc cag gtc gct gag ttc tac ggg gcc aca gag tgc aac tgt
S S R F H I P Q V A E F Y G A T E C N C
1381 agc cgc ggc aac ttc gac agc cag gtc ggg gcc tgt ggt ttc aat agc cgc atc ctg tcc
S L G N P D S Q V G A C G F N S R I L S
1441 ttc gtc tac ccc atc cgg ttg gta cgt gtc aac gag gac acc atg gag ctg atc cgg ggg
F V Y P I R L V R V N E D T M E L I R G
1501 ccc gac ggc gtc tgc att ccc tgc cag cca ggt gag cgg ggc cag ctg gtc ggc cgc atc
P D G V C I P C Q P G E P G Q L V G R I
1561 atc cag aaa gac ccc ctg cgc cgc ttc gat ggc tac ctc aac cag ggc gcc aac aac aag
I Q K D P L R R F D G Y L N Q G A N N K
1621 aag att gcc aag gat gtc ttc aag aag ggg gac cag gcc tac ctt act ggt gat gtc ctg
K I A K D V F K K G D Q A Y L T G D V L
1681 gtc atg gac gag ctg ggc tac ctg ttc cga gac cgc act ggg gac acg ttc cgc tgg
V M D E L G Y L Y F R D R T G D T F R W
1741 aaa ggt gag aac gtc tcc acc acc gag gtc gaa ggc aca ctc agc cgc ctg ctg gac atg
K G E N V S T T E V E G T L S R L L D M
1801 gct gac gtc gcc gtc tat ggt gtc gag gtc cca gga acc gag ggc cgg gcc gga atg gct
A D V A V Y G V E V P G T E G R A G M A
1861 gct gtc gcc agc ccc act ggc aac tgt gac ctg gag cgc ttt gct cag gtc ttg gag aag
A V A S P T G N C D L E R F A Q V L E K
1921 gaa ctg ccc ctg tat ggc cgc ccc atc ttc ctg cgc ctc ctg cct gag ctg cac aca aca
E L P L Y A R P I F L R L L P E L H K T
1981 gga acc tac aag ttc cag aag aca gag cta cgg aag gag ggc ttt gac cgg gct att gtc
G T Y K F Q K T E L R K E G F D P A I V
2041 aaa gac cgg ctg ttc tat cta gat gcc cag aag ggc cgc tac gtc cgg ctg gac caa gag
K D P L F Y L D A Q K G R Y V P L D Q E
2101 gcc tac agc cgc atc cag gca ggc gag gag aag ctg tga ttc ccc cca tcc ctc tga ggg
A Y S R I Q A G E E K L *
2161 cgg ggc gat gct gga tcc gga gcc cca ggt tcc gcc cca gag cgg tcc tgg aca agg cca
2221 gac caa agc aag cag ggc ctg gca cct cca tcc tga ggt gct gcc cct cca tcc aaa act
2281 gcc aag tga ctc att gcc ttc cca acc ctt cca gag gct ttc tgt gaa agt ctc atg tcc
2341 aag ttc cgt ctt ctg ggc tgg gca ggc cct ctg gtt ccc agg ctg aga ctg acg ggt ttt
2401 ctc agg atg atg tct tgg gtc agg gta ggg aga gga caa ggg gtc acc gag ccc ttc cca
2461 gag agc agg gag ctt ata aat gga acc aga gca gaa gtc ccc aga ctc agg aag tca aca
2521 gag tgg gca ggc aca gtc gta gca tcc atc tgg tgg cca aag aga atc gta gcc cca gag
2581 ctg ccc aag ttc act ggg ctc cac ccc cac ctc cag gag ggg agg aga gga cct gac atc
2641 tgt agg tgg ccc ctg atg ccc cat cta cag cag gag gtc agg acc acg ccc ctg gcc tct
2701 ccc cac tcc ccc atc ctc ctc cct ggg tgg ctg cct gat tat ccc tca ggc agg gcc tct
2761 cag tcc ttg tgg gtc tgt gtc acc tcc atc tca gtc ttg gcc tgg cta tga ggg gag gag
2821 gaa tgg gag agg ggg ctc agg ggc caa taa act ctg cct tga gtc ctc cta aaa aaa aaa
2881 aaa aaa aaa aaa aaa aaa aaa ggg cgg cgc c

Figure 27

Protein sequence 646 a.a. MRAPGAGAASVV ... VYTRICSGAFAL

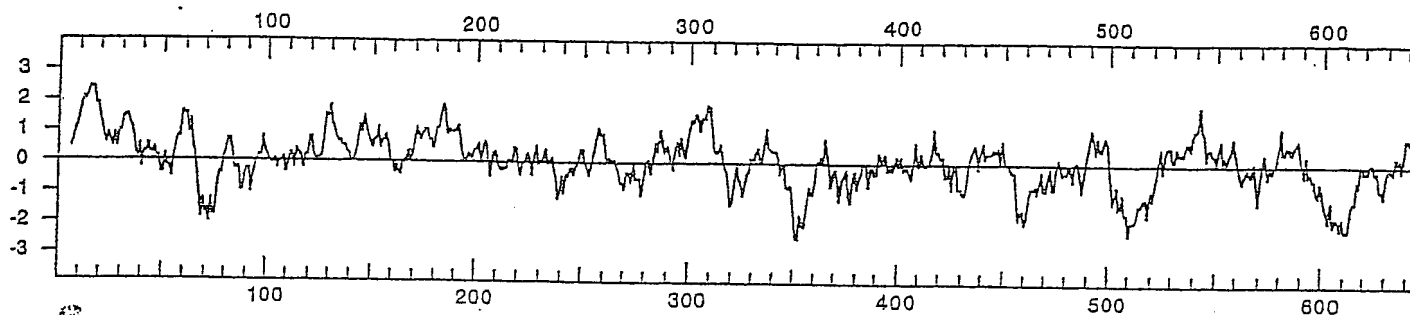


Figure 28A

Protein sequence 646 a.a. MRAPGAGAASVV ... VYTRICSGAFAL

646 Amino Acids MW : 71062 Dalton

		n	n(%)	MW	MW(%)
A	ala alanine	64	9.9	4546	6.4
C	cys cysteine	15	2.3	1545	2.2
D	asp aspartic acid	30	4.6	3450	4.9
E	glu glutamic acid	11	4.8	4000	5.6
F	phe phenylalanine	29	4.5	4264	6.0
G	gly glycine	63	9.8	3592	5.1
H	his histidine	13	2.0	1781	2.5
I	ile isoleucine	29	4.5	3279	4.6
K	lys lysine	22	3.4	2818	4.0
L	leu leucine	77	11.9	8707	12.3
M	met methionine	11	1.7	1441	2.0
N	asn asparagine	15	2.3	1710	2.4
P	pro proline	29	4.5	2814	4.0
Q	gln glutamine	25	3.9	3201	4.5
R	arg arginine	49	7.6	7648	10.8
S	ser serine	33	5.1	2872	4.0
T	thr threonine	27	4.2	2728	3.8
V	val valine	51	7.9	5052	7.1
W	trp tryptophan	9	1.4	1674	2.4
X	ukw unknown	-	-	-	-
Y	tyr tyrosine	24	3.7	3913	5.5
Z	--- STOP	-	-	-	-

Figure 28B

0040550460
16E260"40550460

66E26D*1055D460

rsFATP1 full length protein

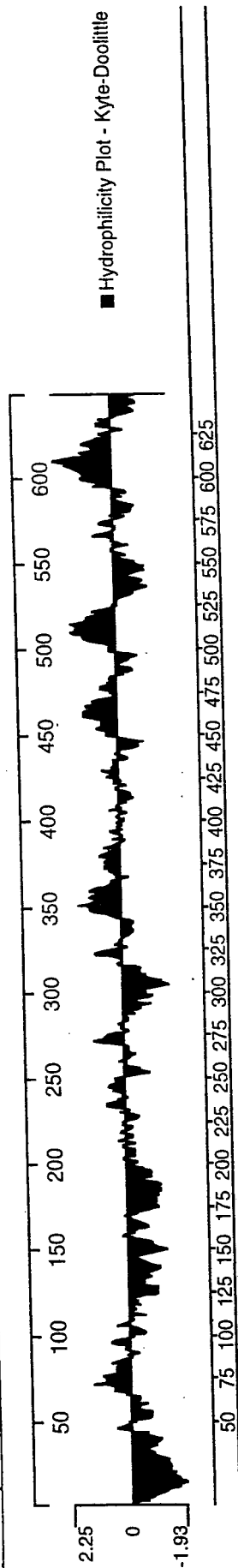


Figure 28C

hsFATP4.pep -> KD Hydrophobicity <11/1>

Protein sequence 643 a.a. MLLGASLVGVLL ... AYSRIQAGEEKL

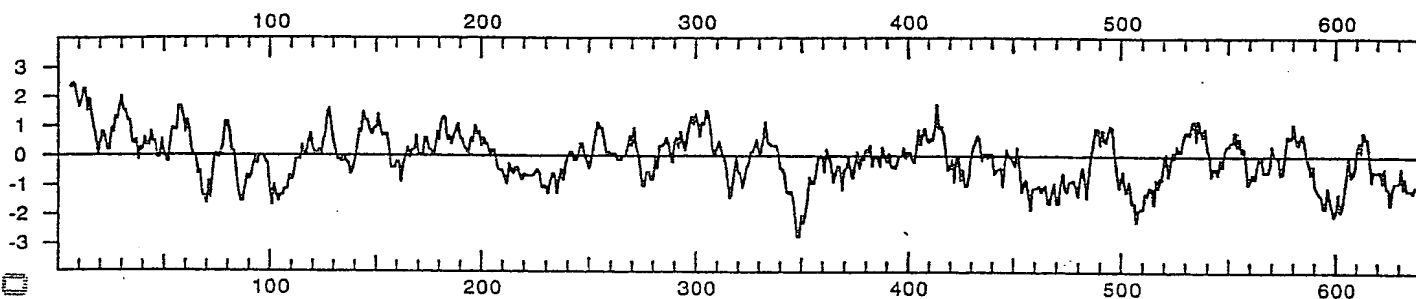


Figure 29A

hsFATP4.pep -> A. A. Usage

Protein sequence 643 a.a. MLLGASLVGVLL ... AYSRIQAGEEKL

643 Amino Acids MW : 72018 Dalton

		n	n(%)	MW	MW(%)
A	ala alanine	46	7.2	3267	4.5
C	cys cysteine	16	2.5	1648	2.3
D	asp aspartic acid	33	5.1	3795	5.3
E	glu glutamic acid	33	5.1	4258	5.9
F	phe phenylalanine	34	5.3	5000	6.9
G	gly glycine	54	8.4	3079	4.3
H	his histidine	12	1.9	1644	2.3
I	ile isoleucine	30	4.7	3392	4.7
K	lys lysine	31	4.8	3970	5.5
L	leu leucine	76	11.8	8594	11.9
M	met methionine	12	1.9	1572	2.2
N	asn asparagine	21	3.3	2394	3.3
P	pro proline	31	4.8	3008	4.2
Q	gln glutamine	23	3.6	2945	4.1
R	arg arginine	45	7.0	7024	9.8
S	ser serine	35	5.4	3046	4.2
T	thr threonine	32	5.0	3233	4.5
V	val valine	46	7.2	4557	6.3
W	trp tryptophan	8	1.2	1488	2.1
X	ukw unknown	-	-	-	-
Y	tyr tyrosine	25	3.9	4076	5.7
Z	--- STOP	-	-	-	-

Figure 29B

66E260" 10550160

hsFATP4 full length. protein

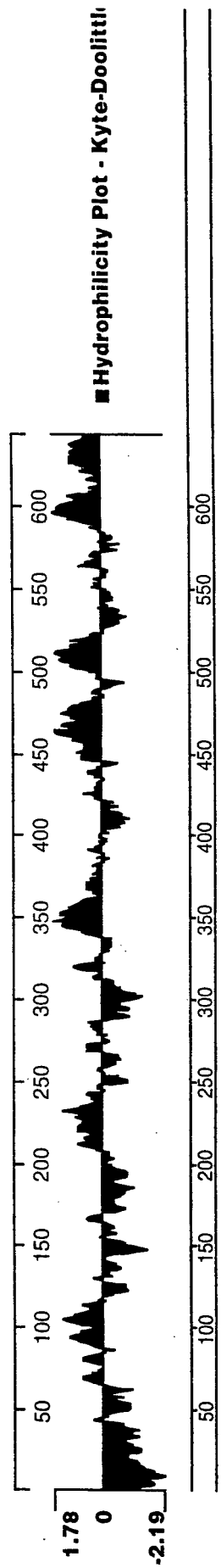


Figure 29C

1 ATGCGGGGCTCC GGGTGGGGGCGGCGCTGGGTGGTCTCGCTGGCGCTGT hFATP1con.seq ORF
1 ATGCGGGGCTCC TGGAGGAGGAAGAGCGCTGTGTGGCTCGCTGGCGCTGT mFATP1.seq ORF (from genomic)

51 GTGGCTGGGGGCT GCGGTGGAGCTGGAGCGCGGGAAGCGGCGCTCGCTGG hFATP1con.seq ORF
51 TTGGCTGGGGGCT TCGGTGGAGCTGGAGCGCGGGAAGCGGCGCTCGCTGG mFATP1.seq ORF (from genomic)

101 GTAGGTGGG CAGCGGGGCTGGGGCTTCTGGG CATCGCTCTGCAAGAC hFATP1con.seq ORF
101 GTAGGTGGG TGGGGGCTGGGGCTTCTGGG CATCGCTCTGCAAGAC mFATP1.seq ORF (from genomic)

151 GCGAGGCGAGACCTCTT CCGTCTCTCTGT GCTGATCCGCGT GCGCTT GGA hFATP1con.seq ORF
151 GCGAGGCGAGACCTCTT TGGCTCTCTCTGT TCTGATTCGTGT TCGCTT AGA mFATP1.seq ORF (from genomic)

201 GCTGGG GCGGACCAAGGTGC CCGCCACAC CATCCCGCGCATCTT TCAGG hFATP1con.seq ORF
201 GCTGGG ACGACACCGGCGAGG AGGAGACAC GATCCCGTGCATCTT CCAGG mFATP1.seq ORF (from genomic)

251 GGGTA GTGAGGAGCA GCGCAGAGGCGCTGGG GCTGGTGA TGGG GGGACC hFATP1con.seq ORF
251 CTGTGCGCCGGGAGCA ACGAGAGCGCTGGG ACTGGTGA CCGG AGTAGT mFATP1.seq ORF (from genomic)

301 GCGAG TGGTGGAGCTT TGGCAGGCTGGAG GCTTACTTCAATGG GGTAGG hFATP1con.seq ORF
301 GGTATA TGGTGGAGCTT CCGACAGGCTGGAG ACCTACTTCAATGG TGTAGG mFATP1.seq ORF (from genomic)

351 CAACCTCTTCCGCGAGCTGGGGCTT CCGGCG GGGCGA CTTGGTGGC CATCT hFATP1con.seq ORF
351 CAACCTGTTCGCGAGCTGGGGCTT TGGACG AGGCGA TGTGGTGGC TGTGT mFATP1.seq ORF (from genomic)

401 TCCTGGAGGGGCGGCGGAGTTCTGTGGG GCTGTGGCTGGGGCTGGGCAAG hFATP1con.seq ORF
401 TCCTGGAGGGGCGGCGGAGTTCTGTGGG ACTGTGGCTGGGGCTGGGCAAG mFATP1.seq ORF (from genomic)

451 GCGGG CATGGAGGCGCGGCT GCTCAA CGTGAACCTG CCGCG CAGAGCCCT hFATP1con.seq ORF
451 GCGGG TGTGGTGGG TGGCTCTTCTCAA TGTCAAACCTG AGGCG GAGAGCCCT mFATP1.seq ORF (from genomic)

501 GGCCTTCTGGCTGGGCACTCGGGCG TAAGGGCT GATCTT TGG AGGAG hFATP1con.seq ORF
501 GGCCTTCTGGCTGGGCACTCGGGCG TAAAGGGCT CATTTATGG CCGGG mFATP1.seq ORF (from genomic)

551 AATGG TGGCGGCGGTGGG CGAAGTGAGCG GGCATCTGGGGA AAGTTTG hFATP1con.seq ORF
551 AGATGG CAGCGGCGGTGGG GGAAGTGAGCG AGCAGCTGGGGA AGAGCTTC mFATP1.seq ORF (from genomic)

601 ATCAAGTTCTGCTCTGGAGA CTGGGGGCGGAGGGCATCTTGGCGGAGACAC hFATP1con.seq ORF
601 CTCAAGTTCTGCTCTGGAGATCTGGGGGCTGAGAGCATCTTGGCTGAGACAC mFATP1.seq ORF (from genomic)

651 CCACTCTCTGGACCGGCTGCT GAAGGAGGGCTGTAGTGGCCCTTGGCAC hFATP1con.seq ORF
651 GCACTCTCTGGACCGGCTGCT TGGCTGAGGGGCGCACCAACCGCTTGGCAC mFATP1.seq ORF (from genomic)

701 AGATCC CAGCAAGGGCATGGACGATCGTCTTTTCTACATCTACACGTGG hFATP1con.seq ORF
701 AAGCCCAGGCAAGGGCATGGATGATCGGCTGTTTCTACATCTATACCTGG mFATP1.seq ORF (from genomic)

751 GGGACCAACCGGCTTGGCAAGGCTGGCATTTGT CGTGCAACAGCAGGTACTA hFATP1con.seq ORF
751 GGGACCAACCGGCTTGGCAAGGCTGGCATTTGT GGTGCAACAGCAGGTACTA mFATP1.seq ORF (from genomic)

801 CCGCATGGAGGCTTCTGGCCACCA CGCTACCGCATGCAAGGCGCTGACG hFATP1con.seq ORF
801 CCGCATTGGTGGCTTCTGGCCACCA TCCCTACAGCATGCGT GCGCGCGATG mFATP1.seq ORF (from genomic)

851 TGCTCTATGACTGCTGCGCCTGTACCACTCGGCGGAAACATCAT CCGC hFATP1con.seq ORF
851 TGCTCTATGACTGCTGCGCCTGTACCACTCGGCGGAAACATCAT GGGT mFATP1.seq ORF (from genomic)

901 GTGGGGCAGTGTCTCATCTATGGGCTGAGAGTCTCTCTCGGCAAGAAATT hFATP1con.seq ORF
901 GTGGGGCAGTGTCTCATCTACGGGCTGAGAGTCTCTCTCGGCAAGAAATT mFATP1.seq ORF (from genomic)

951 CTCGGGCGAGCGCTTCTGGGA CAGCTGCATCAAGTACAACTGGCAGGTG hFATP1con.seq ORF
951 CTCGGGCGAGCGCTTCTGGGA TGACTGTGTCAAAGTACAACTGGCAGGTG mFATP1.seq ORF (from genomic)

1001 TCAAGTACATCGGGGAGATCTGCGGCTACCTGCTGA AGCAGCGGGTGGCG hFATP1con.seq ORF
1001 TCAAGTACATAGGTGA AATCTGCGGCTACCTGCTGA GGCAGCGGGTGGCG mFATP1.seq ORF (from genomic)

1051 GAGCGGGAGAGGCGACACCGCGTGGCGCTGGG GGTGGG GAA CCGGGCTGG hFATP1con.seq ORF
1051 GAGCGGGAGAGGCGACACCGCGTGGCGCTGGG CGTGGG TAA TGGGCTGG mFATP1.seq ORF (from genomic)

1101 TCTGCCATCTGGGAGGAGTTCAAG GAGCGCTTGGCGCTAGGCCAATCG hFATP1con.seq ORF
1101 GCGAGCATCTGGGAGGAGTTCAAG CAGCGCTTGGCGCTAGGCCAATCG mFATP1.seq ORF (from genomic)

1151 GGGAGTTCTACGGCG CACCGAGTGCAACTGCAGCATTTGCCAACATGGAC hFATP1con.seq ORF
1151 GCGAGTTCTACGGCG TACCGAGTGCAACTGCAGCATTTGCCAACATGGAC mFATP1.seq ORF (from genomic)

1201 GCGAAGGTGGGCTCTTGGT TTTCAACAGCGCATCTTGGCGCCACGTCTA hFATP1con.seq ORF
1201 GCGAAGGTGGGCTCTTGGT CTTCAACAGCGCATCTTGGCGCCACGTCTA mFATP1.seq ORF (from genomic)

1251 CCGCATCGGCTGGTGAAGGTCAATGAGGACAAATGGAGG TGGCTGGGG hFATP1con.seq ORF
1251 CCGCATCGGCTGGTGAAGGTCAATGAGGACAAATGGAGG CACTGGGG mFATP1.seq ORF (from genomic)

1301 ATGCGCAGGGGCTCTGCATCCGCTGGCGAGGCCGGGGAGGCTGGGCTCTT hFATP1con.seq ORF
1301 ATGCGCAGGGGCTCTGCATCCGCTGGCGAGGCCGGGGAGGCTGGGCTCTT mFATP1.seq ORF (from genomic)

FIG. 30A

[illegible]

1620 TGG TGT GGC CAG CCG CTTG GCGTCTGTGACCTGAG CCGCTTGG TCAAG GTCTTGGA GAGA hsFATP4
 1620 LGG CGT TGC AAG TTCCG TCA GCAACCTGTGTGCTGCTGAG ACGCATTGG ACGAG ACCTCTG AAGA mmFATP4
 1680 GGA ACTGTG CCGTCTATGG GCGGGCGGCTCTCTGCGCTCTC CTTC CTGGCGTGAAGCTGCACAA AAGA hsFATP4
 1680 GGG GCTCG TCTCTCAATGG CCGCGGGTCTCTGCGCTCTC TTTC TTACCTGTGGCTGCAACAA GAGA mmFATP4
 1740 AGG AAGGT ACAAATCCAGAGACAGAG CT ACGG GGGGGCGCTTGTGACGG GGGCT AATTG hsFATP4
 1740 AAG GACCT TGAACCTCCAGAAAG CAGAGT G GCGCAAGGAGCGCTCTGACCG AATCA GSTTG mmFATP4
 1800 GAAAGACCCCGCTCTTAACT AGATTC C AAGA GCGG CCGCTTCCT CCG GCTGACCA AAGA hsFATP4
 1800 GAAGA CCGCGCTGTCTATAT GATTC TGGGAGGAG TCGTACCT CCG GCTGACCA AAGA mmFATP4
 1860 GGCCT CA GCGGCATTCAGGCAAGGAGG CAAAGCTC hsFATP4
 1860 GGTCT TGC CCGCTCCAGGCAAGGAGG CAAAGCTC mmFATP4
 Decoration 'Decoration #1: shadow'

Decoration 'Decoration #1': Shade (with solid bright yellow) residues that match the consensus named 'Consensus #1' exactly.

Figure 31B

09405604-092346

1	HTCAFGAGAAISV	VSEALATL	L	EGDREWTSATATA	L	GAIVIC	S	IGWRERHRAV	CT	TAAR	DD	FG	DS	V	hsFAT1pep
1	MHAAPGAGTASV	ASLALATL	F	EGDREWTSATATA	F	CAVVIC	G	IGWRERHRAV	CT	TAAR	DD	FG	DS	V	mmFAT1pep
61	ELRVRLEERPH	QRRAG	H	ETLR	R	EQAN	V	Q	Q	Q	Q	Q	Q	Q	hsFAT1pep
61	ELRVRLEERPH	QRRAG	H	ETLR	R	EQAN	V	Q	Q	Q	Q	Q	Q	Q	mmFAT1pep
121	RQDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
121	RQDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
181	FQDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
181	FQDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
241	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
241	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
301	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
301	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
361	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
361	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
421	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
421	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
481	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
481	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
541	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
541	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep
601	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	hsFAT1pep
601	QDLPAPEDAVIA	I	ETLR	Q	R	P	P	P	P	P	P	P	P	P	mmFAT1pep

Decoration 'Decoration #2': Shade (with solid bright yellow) residues that match the consensus named 'Consensus #1' exactly.

Figure 32

Operation 'Decoration #1': Shade (with solid bright yellow) residues that match the consensus named 'Consensus #1' exactly.

U.S. DEPARTMENT OF AGRICULTURE

Figure 33

hsFATP6

```

1 aac ggc aag taa gcg caa cgc aat taa tgt gag tag ctc act cat tag gca ccc cag gct
61 tta cac ttt atg ctt ccg ggc tcg tat gtt gtg tgg aat tgt gag cgg ata cca att tca
121 cac agg aac cag cta tga cat gat tac gaa ttt aat acg act cac tat agg gaa ttt ggc
181 cct cga ggc caa gaa ttc ggc acg agg ggt gct gag ccc ctg cgc ggt ttc tgg tgc gta
241 gag act gta aat cgc tgc gct tct cag tca tca tca tcc cag ctt ttc ccg gct cga att
301 cag cct cca act caa gct cgc ggc aaa gac tac ctg aga gga gaa aag ctt ctg tcc ctg
361 gac ctt ctt ctg agg gtg gag tcg gag gct ccc tgc ttt cca gcc gcc cag tga ccc aag
421 ctt aat ctt cag cac cac ttg ggg cga cct ttc cgg tgc aaa cct acg att ctg ttt ctc
481 agg act cct ccc cat ccc gct tcg ccc cgg aaa agc tga caa gaa ctt cag gtg taa gcc
541 ctg agt agt gag gat ctg cgg tct ccc tgg aga gct gtg cct gga aga gaa gga cgc tgg
601 tgg ggg ctg aga tca gag ctg tct tct ggc cca gtt gcc ccc atg ctt ctg tca tgg cta

M L L S W L
661 aca gtt cta ggg gct gga atg gtc gtc ctg cac ttc ttg cag aaa ctc ctg ttc cct tac
T V L G A G M V V L H F L Q K L L F P Y
721 ttt tgg gat gac ttc tgg ttc gtg ttg aag gtg gtg ctc att ata att cgg ctg aag aag
F W D D F W F V L K V V L I I I R L K K
781 tat gaa aag aga ggg gag ctg gtg act gtg ctg gat aaa ttc ttg agt cat gcc aaa aga
Y E K R G E L V T V L D K F L S H A K R
841 caa cct cgg aaa cct ttc atc atc tat gag gga gac atc tac acc tat cag gat gta gac
Q P R K P F I I Y E G D I Y T Y Q D V D
901 aaa agg agc agc aga ggc gcc cat gtc ttc ctg aac cat tcc tct ctg aaa aag ggg gac
K R S S R V A H V P L N H S S L K K G D
961 acg gtg gct ctg ctg atg agc aat gag ccg gac ttc gtt cac gtg tgg ttc ggc ctc gcc
T V A L L M S N E P D F V H V W F G L A
1021 aag ctg ggc tgc gtg gtg gcc ttt ctc aac acc aac att cgc tcc aac tcc ctc ctg aat
K L G C V V A F L N T N I R S N S L L N
1081 tgc atc cgc gcc tgt ggg ccc aga gcc cta gtg gtg ggc gca gat ttg ctt gga acg gta
C I R A C G P R A L V V G A D L L G T V
1141 gaa gaa atc ctt cca agc ctc tca gaa aat atc agt gtt tgg ggg atg aaa gat tct gtt
E E I L P S L S E N I S V W G M K D S V
1201 cca caa ggt gta att tca ctc aaa gaa aaa ctg agc acc tca cct gat gag ccc gtg cca
P Q G V I S L K E K L S T S P D E P V P
1261 cgc agc cac cat gtt gtc tca ctc ctc aag tct act tgt ctt tac att ttt acc tct gga
R S H H V V S L L K S T C L Y I F T S G
1321 aca aca ggt cta cca aaa gca gct gtg att agt cag ctg cag gtt tta agg ggt tct gct
T G L P K A A V I S Q L Q V L R G S A
1381 gtc ctg tgg gct ttt ggt tgt act gct cat gac att gtt tat ata acc ctt ctt ctg tat
V L W A F G C T A H D I V Y I T L P L Y
1441 cat agt tca gca gct atc ctg gga att tct gga tgt gtt gag ttg ggt gcc act tgt gtg
H S S A A I L G I S G C V E L G A T C V
1501 tta aag aag aaa ttt tca gca agc cag ttt tgg agt gac tgc aag aag tat gat gtg act
L K K K F S A S Q F W S D C K K Y D V T
1561 gtg ttt cag tat att gga gaa ctt tgt cgc tac ctt tgc aaa caa tct aag aga gaa gga
V F Q Y I G E L C R Y L C K Q S K R E G
1621 gaa aag gat cat aag gtg cgt ttg gca att gga aat ggc ata cgg agt gat gta tgg aga
E K D H K V R L A I G N G I R S D V W R
1681 gaa ttt tta gac aga ttt gga aat ata aag gtg tgt gaa ctt tat gca gct acc gaa tca
E F L D R F G N I K V C E L Y A A T E S
1741 agc ata tct ttc atg aac tac act ggg aga att gga gca att ggg aga aca aat ttg ttt
S I S F M N Y T G R I G A I G R T N L F
1801 tac aaa ctt ctt tcc act ttt gac tta ata aag tat gac ctt cag aaa gat gaa ccc atg
Y K L L S T F D L I K Y D F Q K D E P M
1861 aga aat gag cag ggt tgg tgt att cat gtg aaa aaa gga gaa cct gga ctt ctc att tct
R N E Q G W C I H V K K G E P G L L I S
1921 cga gtg aat gca aaa aat ccc ttc ttt ggc tat gct ggg cct tat aag cac aca aaa gac
R V N A K N P F F G Y A G P Y K H T K D
1981 aaa tbg ctt tgt gat gtt ttt aag aag gga gat gtt tac ctt aat act gga gac tta ata
K L L C D V F K K G D V Y L N T G D L I
2041 gtc cag gat cag gac aat ttc ctt tat ttt tgg gac cgt act gga gac act ttc aga tgg
V Q D Q D N F L Y F W D R T G D T F R W
2101 aaa gga gaa aat gtc gca acc act gag gtt gct gat gtt att gga atg ttg gat ttc ata
K G E N V A T T E V A D V I G M L D F I
2161 cag gaa gca aac gtc tat ggt gtg gct ata tca ggt tat gaa gga aga gca gga atg gct
Q E A N V Y G V A I S G Y E G R A G M A
2221 tct att att tta aaa cca aat aca tct tta gat ttg gaa aaa gtt tat gaa caa gtt gta
S I I L K P N T S L D L E K V Y E Q V V
2281 aca ttt cta cca gct tat gct tgt cca cga ttt tta aga att cag gaa aaa atg gaa gca
T F L P A Y A C P R F L R I Q E K M E A
2341 aca gga aca ttc aaa cta ttg aag cat cag ttg gtg gaa gat gga ttt aat cca ctg aaa
T G T F K L L K H Q L V E D G F N P L K
2401 att tct gaa cca ctt tac ttc atg gat aac ttg aaa aag tct tat gtt cta ctg acc agg
I S E P L Y F M D N L K K S Y V L L T R
2461 gaa ctt tat gat caa ata atg tta ggg gaa ata aaa ctt taa gat ttt tat atc tag aac
E L Y D Q I M L G E I K L
2521 ttt cat atg ctt tct tag gaa gag tga gag ggg ggt ata tga ttc ttt atg aaa tgg gga
2581 aag gga gct aac att aat tat gca tgt act ata ttt cct taa tat gag aga taa ttt ttt
2641 aat tgc ata aga att tta att tct ttt aat tga tat aaa cat tag ttg att att ctt ttt
2701 atc tac ttg gag att cag tgc ata act aag tat ttt cct taa tac taa aga ttt taa ata
2761 ata aat agt ggc tag cgg ttt gga caa tca cta aaa atg tac ttt cta ata agt aaa att
2821 tct aat ttt gaa taa aag att aaa ttt tac tga aaa aaa aaa aaa aaa aaa ttt ggc
2881 gcc gc

```

Figure 34

Protein sequence 619 a.a. MLLSWLTVLGAG ... LYDQIMLGEIKL

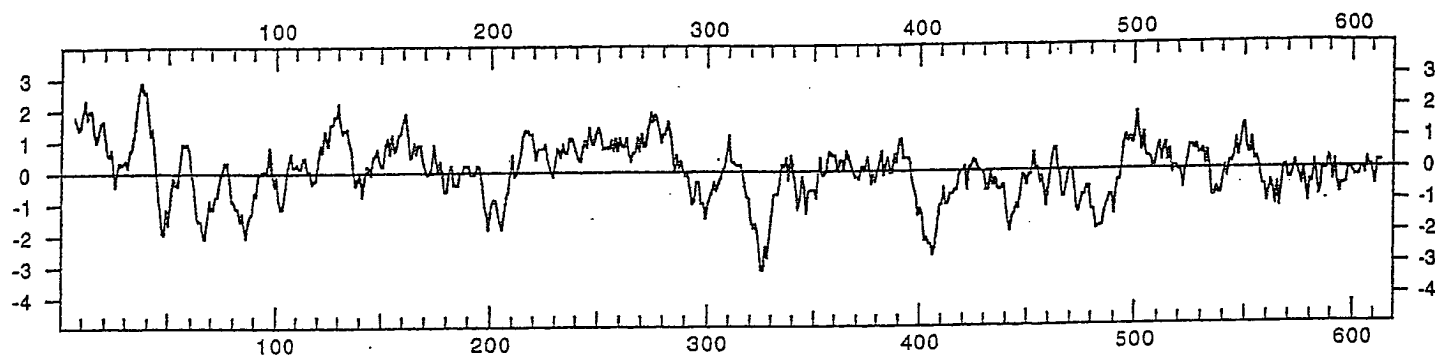


FIGURE 35 A

Protein sequence 619 a.a. MLLSWLTVLGAG ... LYDQIMLGEIKL

619 Amino Acids MW : 70066 Dalton

	n	n(%)	MW	MW(%)
A ala alanine	33	5.3	2344	3.3
C cys cysteine	14	2.3	1442	2.1
D asp aspartic acid	34	5.5	3910	5.6
E glu glutamic acid	31	5.0	4000	5.7
F phe phenylalanine	34	5.5	5000	7.1
G gly glycine	44	7.1	2508	3.6
H his histidine	13	2.1	1781	2.5
I ile isoleucine	37	6.0	4184	6.0
K lys lysine	48	7.8	6148	8.8
L leu leucine	75	12.1	8481	12.1
M met methionine	11	1.8	1441	2.1
N asn asparagine	21	3.4	2394	3.4
P pro proline	21	3.4	2038	2.9
Q gln glutamine	18	2.9	2305	3.3
R arg arginine	27	4.4	4214	6.0
S ser serine	40	6.5	3481	5.0
T thr threonine	30	4.8	3031	4.3
V val valine	51	8.2	5052	7.2
W trp tryptophan	11	1.8	2046	2.9
X ukw unknown	-	-	-	-
Y tyr tyrosine	26	4.2	4239	6.1
Z --- STOP	-	-	-	-

FIGURE 35 B

66260"4050460

isFATP6 full length protein

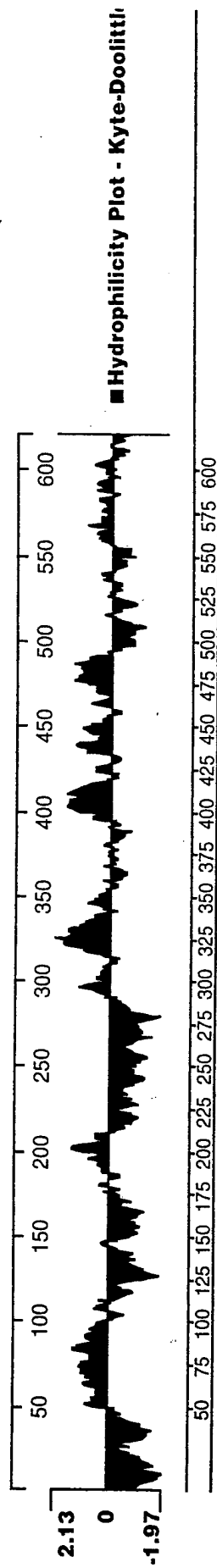


Figure 35C

1	MRAP--GAGASV	SLALWLG	FWLW	SAAAA	GV	VGS	GWR	IRIVC	K	A	R	B	L	E	G	L	hsFATP1pep
1	L	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	hsFATP4pep
1	LLSWLTVL	GM	V	HF	QK	L	F	Y	F	DD	---	---	---	---	---	---	hsFATP6pep
59	S	V	R	R	E	L	R	H	Q	R	A	G	H	I	R	I	hsFATP1pep
45	L	V	L	K	K	A	V	Q	C	L	Q	R	R	T	V	I	hsFATP4pep
38	-	V	L	I	I	R	L	K	Y	E	K	R	G	L	V	L	hsFATP6pep
119	-	L	F	R	Q	L	G	F	P	C	D	V	A	T	L	E	hsFATP1pep
105	-	Q	A	R	C	L	A	S	G	D	M	A	A	T	E	M	hsFATP4pep
95	V	E	N	H	S	S	K	K	G	D	T	V	A	L	L	S	hsFATP6pep
178	A	D	I	E	G	G	D	V	A	A	A	B	S	G	H	G	hsFATP1pep
165	A	D	V	G	S	R	E	M	A	S	A	I	C	B	H	A	hsFATP4pep
155	A	L	V	V	A	D	L	L	G	T	E	E	I	L	S	S	hsFATP6pep
238	K	G	---	M	D	R	L	E	V	Y	A	S	G	T	T	G	hsFATP1pep
224	K	G	---	F	T	D	K	L	E	V	Y	A	S	G	T	T	hsFATP4pep
211	V	V	S	L	L	K	S	T	C	L	V	I	F	T	S	G	hsFATP6pep
296	G	I	I	G	V	G	C	I	Y	L	L	V	D	R	K	K	hsFATP1pep
282	G	N	I	V	G	I	G	C	L	H	G	M	V	M	I	R	hsFATP4pep
270	A	A	L	L	I	S	G	E	V	L	G	A	T	C	V	L	hsFATP6pep
356	H	R	V	R	L	A	V	C	N	G	L	R	P	A	W	E	hsFATP1pep
342	H	Q	M	R	M	A	L	G	N	G	L	R	O	S	I	T	hsFATP4pep
330	H	K	V	R	L	A	I	C	N	G	I	R	S	D	V	R	hsFATP6pep
416	V	Y	P	T	R	L	V	E	V	N	E	D	T	M	E	L	hsFATP1pep
403	M	A	P	T	R	L	V	E	V	N	E	D	T	M	E	L	hsFATP4pep
396	L	S	T	F	D	I	K	Y	D	F	Q	K	D	E	P	M	hsFATP6pep
475	K	I	A	H	S	W	A	S	K	G	D	S	A	Y	T	-	hsFATP1pep
461	K	I	A	K	D	V	P	K	G	D	Q	A	N	G	-	-	hsFATP4pep
447	K	L	L	C	D	V	E	K	K	S	D	-	V	E	N	T	hsFATP6pep
534	Q	T	D	V	A	V	G	V	A	V	S	G	V	E	G	K	hsFATP1pep
520	M	A	D	V	A	V	G	V	E	V	P	G	T	E	C	R	hsFATP4pep
506	I	Q	E	A	N	V	G	V	A	I	S	G	Y	E	G	R	hsFATP6pep
591	T	T	G	T	R	K	I	Q	K	T	R	I	Q	R	E	G	hsFATP1pep
579	K	T	G	T	Y	N	F	Q	K	T	E	R	K	E	G	F	hsFATP4pep
566	A	T	G	T	P	L	L	K	H	Q	L	V	E	D	G	E	hsFATP6pep

Decoration 'Decoration #1': Shade (with solid bright yellow) residues that match the Consensus exactly.

Figure 36

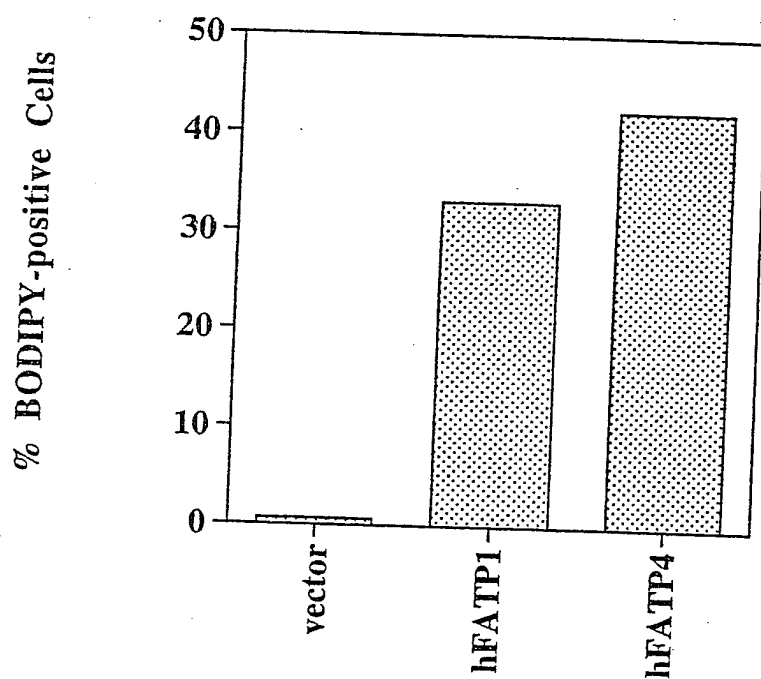
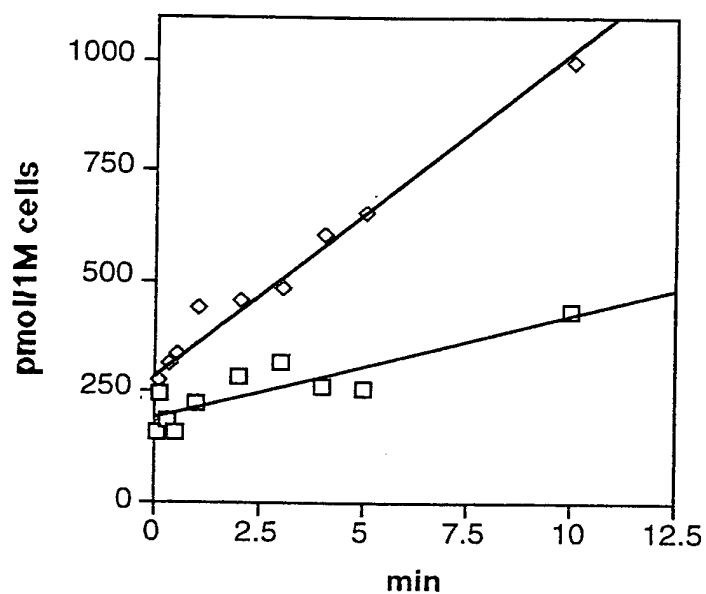


Figure 37



- 293 vector control: 23 pmol/(min*1*10⁶ cells)
◇ 293 FATP4 clone 7: 73 pmol/(min*1*10⁶ cells)

Fig. 38

hsFATP4	1	RIE -	LAAPLVGVLEFCKL -	VLKLPWTFQVGFELL	FLYEGG	GVNFI	VE
mmFATP4	1	RIE -	LAAPLVGVLEFCKL -	VLKLPWTFQVGFELL	FLYEGG	GVNFI	VE
hsFATP1	1	RIAP	GAASVSLALL	WLLGL	PWTWSAAAA	GVV	FLIV
hsFATP4	46	IKTI	IVHLL	FTGGL	LVLEFV	AKVH	OCLOER
mmFATP4	46	IKTI	IVHLL	FTGGL	LVLEFV	AKVH	OCLOER
hsFATP1	48	CKT	IVHLL	FTGGL	LVLEFV	AKVH	OCLOER
hsFATP4	93	IFED	STHTWTF	FRGL	LEFV	GVNFI	VE
mmFATP4	93	IFED	STHTWTF	FRGL	LEFV	GVNFI	VE
hsFATP1	95	VD	AL	TGEC	WTF	AKVH	OCLOER
hsFATP4	140	IVL	LVH	AKVH	OCLOER	RTVFI	ILFAST
mmFATP4	140	IVL	LVH	AKVH	OCLOER	RTVFI	ILFAST
hsFATP1	142	IVL	LVH	AKVH	OCLOER	RTVFI	ILFAST
hsFATP4	187	ICE	FA	DE	ET	GA	VPE
mmFATP4	187	ICE	FA	DE	ET	GA	VPE
hsFATP1	189	VA	SGH	GK	IK	DL	GL
hsFATP4	233	PD	KG	FT	DR	LE	FT
mmFATP4	233	PD	KG	FT	DR	LE	FT
hsFATP1	236	PD	KG	FT	DR	LE	FT
hsFATP4	280	Q	IV	YD	CE	PL	YH
mmFATP4	280	Q	IV	YD	CE	PL	YH
hsFATP1	283	Q	IV	YD	CE	PL	YH
hsFATP4	327	NC	IV	YD	CE	PL	YH
mmFATP4	327	NC	IV	YD	CE	PL	YH
hsFATP1	330	NC	IV	YD	CE	PL	YH
hsFATP4	374	PF	FI	PO	VA	FT	YD
mmFATP4	374	PF	FI	PO	VA	FT	YD
hsFATP1	377	PF	FI	PO	VA	FT	YD
hsFATP4	421	VN	ED	TH	EL	TH	EL
mmFATP4	421	VN	ED	TH	EL	TH	EL
hsFATP1	424	VN	ED	TH	EL	TH	EL
hsFATP4	468	AN	NK	RI	AK	CV	PK
mmFATP4	468	AN	NK	RI	AK	CV	PK
hsFATP1	471	AN	NK	RI	AK	CV	PK
hsFATP4	515	AV	GT	TE	VE	GT	TE
mmFATP4	515	AV	GT	TE	VE	GT	TE
hsFATP1	518	AV	GT	TE	VE	GT	TE
hsFATP4	562	LE	RI	FA	QV	LE	KE
mmFATP4	562	LE	RI	FA	QV	LE	KE
hsFATP1	565	PN	AI	YD	EL	ON	VL
hsFATP4	609	A	IV	KE	RL	FL	YD
mmFATP4	609	A	IV	KE	RL	FL	YD
hsFATP1	612	R	Q	TS	RI	FL	YD

Fig. 39

Fig. 40

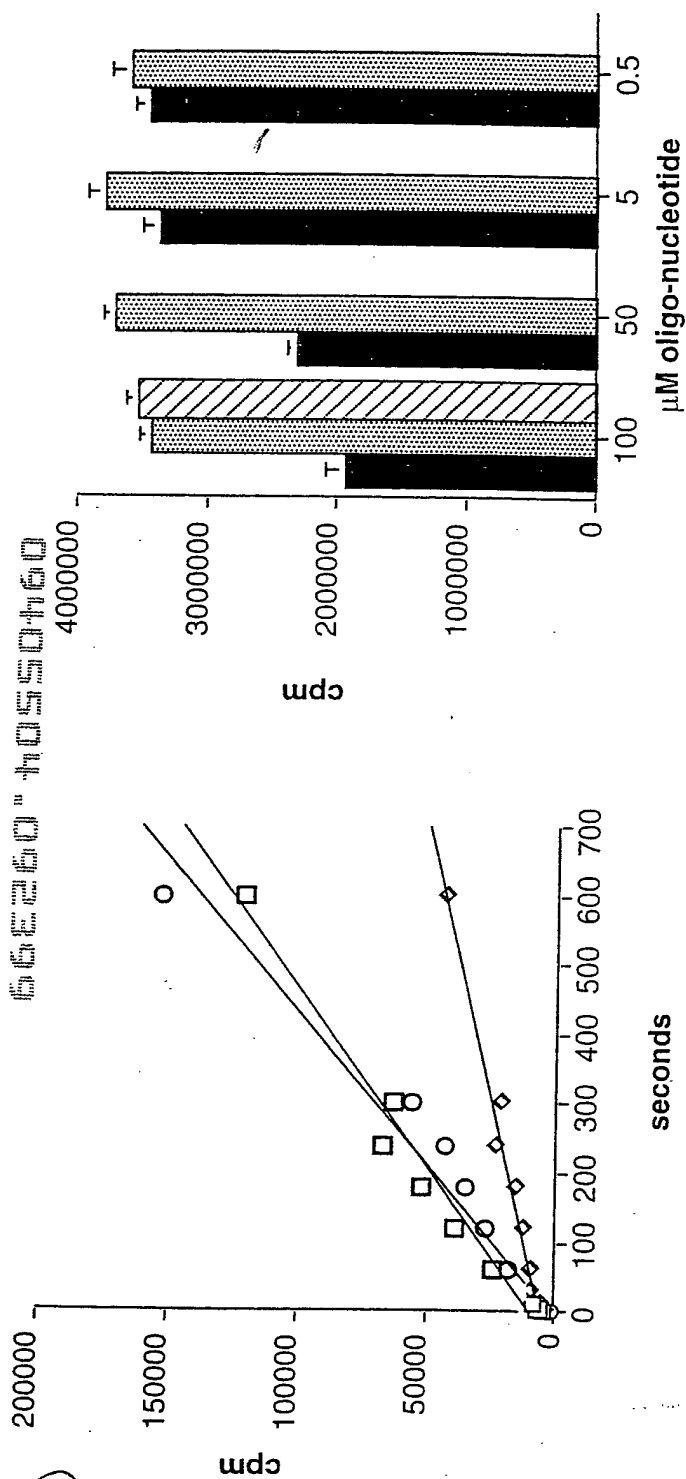


Fig. 41

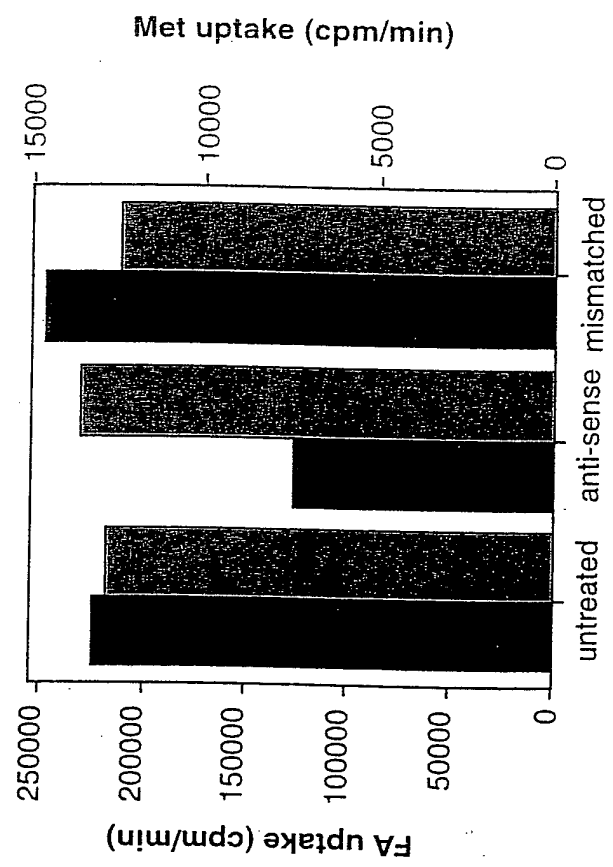
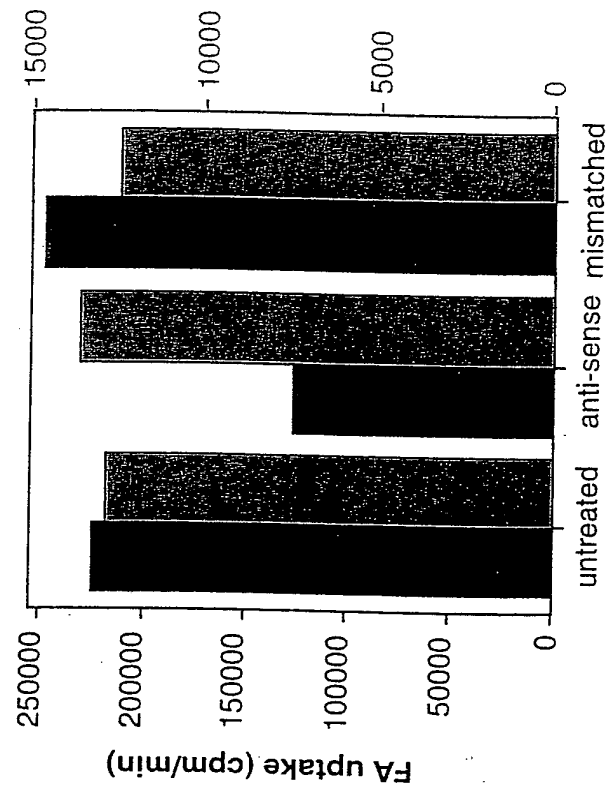


Fig. 42



hsFATP1 full lenght.DNA

1

10 20 30 40

TCGACCCACGGCGTCCGGGACCCCAAAGCAGAAGCCCGCA 40
 CAGTAGGCACAGCGCACCCAAGAAGGGTCCAGGAGTCTGC 80
 AGAAACAGAAAGGTCCCCGGCCTCAGCCTCCTAGTCCCTG 120
 CCTGCCTCCTGCCTGAGCTTCTGGGAGACTGAAGGCACGG 160
 CTTGCAGCTTCAGGATGCGGGCTCCGGGTGCGGGCGCGGC 200

210 220 230 240

CTCGGTGGTCTCGCTGGCGCTGTTGTGGCTGCTGGGGCTG 240
 CCGTGGACCTGGAGCGCGGCAGCGGCGCTCGGCGTGTACG 280
 TGGGCAGCGGGCTGGCGCTTCTGCGCATCGTCTGCAA 320
 GACCGCGAGGCGAGACCTCTTCGGTCTCTCTGTGCTGATC 360
 CGCGTGCCTGAGCTGCGGGCGCACCGAGCGTGCCGGCC 400

410 420 430 440

ACACCATCCCGCGCATCTTTCAGGCGGTAGTGACGCGACA 440
 GCCCCAGCGCCTGGCGCTGGTGGATGCCGGGACCGGCGAG 480
 TGCTGGACCTTTGCGCAGCTGGACGCTACTCCAATGCGG 520
 TAGCCAACCTCTTCCGCCAGCTGGGCTTCGCGCCGGGCGA 560
 CGTGGTGGCCATCTTCTGGAGGGCCGGCCGGAGTTCGTG 600

610 620 630 640

GGGCTGTGGCTGGGCCTGGCCAAGGCGGGCATGGAGGCCG 640
 CGCTGCTCAACGTGAACCTGCGGCGCGAGCCCCTGGCCTT 680
 CTGCCTGGGCACCTCGGGCGCTAAGGCCCTGATCTTTGGA 720
 GGAGAAAATGGTGGCGGCGGTGGCCGAAGTGAGCGGGCATC 760
 TGGGGAAAAGTTTGATCAAGTTCTGCTCTGGAGACTTGGG 800

810 820 830 840

GCCCCAGGGCATCTTGCCGGACACCCACCTCCTGGACCCG 840
 CTGCTGAAGGAGGCCTCTACTGCCCCCTTGGCACAGATCC 880
 CCAGCAAGGGCATGGACGATCGTCTTTTCTACATCTACAC 920
 GTCGGGGACCACCGGGCTGCCCAAGGCTGCCATTGTCTGTG 960
 CACAGCAGGTACTACCGCATGGCAGCCTTCGGCCACCACG 1000

1010 1020 1030 1040

CCTACCGCATGCAGGCGGCTGACGTGCTCTATGACTGCCT 1040
 GCCCCTGTACCACTCGGCAGGAAACATCATCGGCGTGGGG 1080
 CAGTGTCTCATCTATGGGCTGACAGTCGTCTCCGCAAGA 1120
 AATTCTCGGCCAGCCGCTTCTGGGACGACTGCATCAAGTA 1160
 CAACTGCACGGTGGTTTCACTACATCGGGGAGATCTGCCGC 1200

Fig. 44A

66260"4050460

hsFATP1 full lenght.DNA

```

      1210      1220      1230      1240
      |-----|
TACCTGCTGAAGCAGCCGGTGCGCGAGGCGGAGAGGCGAC 1240
ACCGCGTGCGCCTGGCGGTGGGGAACGGGCTGCGTCCTGC 1280
CATCTGGGAGGAGTTCACGGAGCGCTTCGGCGTACGCCAA 1320
ATCGGGGAGTTCTACGGCGCCACCGAGTGCAACTGCAGCA 1360
TTGCCAACATGGACGGCAAGGTCGGCTCCTGTGGTTTCAA 1400

      1410      1420      1430      1440
      |-----|
CAGCCGCATCCTGCCCCACGTGTACCCCATCCGGCTGGTG 1440
AAGGTCAATGAGGACACAATGGAGCTGCTGCGGGATGCC 1480
AGGGCCTCTGCATCCCCTGCCAGGCCGGGAGCCTGGCCT 1520
CCTTGTGGGTGAGATCAACCAACAGGACCCGCTGCGCCGC 1560
TTCGATGGCTATGTCAGCGAGAGCGCCACCAGCAAGAAGA 1600

      1610      1620      1630      1640
      |-----|
TCGCCCCACAGCGTCTTCAGCAAGGGCGACAGCGCCTACCT 1640
CTCAGGTGACGTGCTAGTGATGGATGAGCTGGGCTACATG 1680
TACTTCCGGGACCGTAGCGGGGACACCTTCCGCTGGCGAG 1720
GGGAGAACGTCTCCACCACCGAGGTGGAGGGCGTGCTGAG 1760
CCGCCTGCTGGGCCAGACAGACGTGGCCGTCTATGGGGTG 1800

      1810      1820      1830      1840
      |-----|
GCTGTTCCAGGAGTGAGGGGTAAGGCAGGGATGGCGGCCG 1840
TCGCAGACCCCCACAGCCTGCTGGACCCCAACGCGATATA 1880
CCAGGAGCTGCAGAAGGTGCTGGCACCCCTATGCCCGGCC 1920
ATCTTCTGCGCCTCCTGCCCCAGGTGGACACCACAGGCA 1960
CCTTCAAGATCCAGAAGACGAGGGCTGCAGCGAGAGGGCTT 2000

      2010      2020      2030      2040
      |-----|
TGACCACGCCAGACCTCAGACCGGCTCTTCTTCCTGGAC 2040
CTGAAGCAGGGCCACTACCTGCCCTTAAATGAGGCACTCT 2080
ACACTCGCATCTGCTCGGGCGCCTTCGCCCTCTGAAGCTG 2120
TTCCTCTACTGGCCACAACTCTGGGCCTGGTGGGAGAGG 2160
CCAGCTTGAGCCAGACAGCGCTGCCCAGGGGTGGCCGCCT 2200

      2210      2220      2230      2240
      |-----|
AGTACACACCCACCTGGCCGAGCTGTACCTGGCACGGCCC 2240
ATCCTGGACTGAGAACTGGAACCTCAGAGGAACCCGTGC 2280
CTCTCTGCTGCCTTGGTGCCCCCTGTGTCTGCCTCCTCTCC 2320
CTGCTTTTTCAGCCTCTGTCTCCTTCCATCCCTGTCCCTGT 2360
CTGGCCTTAACCTCTTCCCTCTTTTCTTTTCTTTCTTTCT 2400

      2410      2420      2430      2440
      |-----|
TTCTTTTTTTTTAAGATAGAGTCTCACTCTGCTGCCCGGG 2440
CTAGAGTGCACTGGTGGGATCTCGGCTCACTGCAACCTCT 2480
GCCTCCTGGGGTTCAAGTGATCCTCCCACCTCAGCCTCCT 2520
GAGTAGCTGGGATTACAGGCACCCGCCACCACGTCCAGCT 2560
AATTTTATATTTTATAGTAGAGACGGGGTTTACCATGTT 2600

```

Fig. 44B

09405504-09399

hsFATP1 full lenght.DNA

2610 2620 2630 2640
 GGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCCGC 2640
 TGGCCTCGGCCTCCCAGAGTGCTGGGATTATAGGCGTGAG 2680
 CCTCTGGCCCGGCCTTTCTTTTTCTCTCCTCTCCTGCC 2720
 GAGAGTGGAACACACGTGTCCTGGGAGCTGCATCTTGTGT 2760
 AGGGTCCAGCTGCTTTTGGGGACTGCAGGAATCATCTCCC 2800
 2810 2820 2830 2840
 CTGGGCCCTGGACTCGGACTGGGGCCTCCCCACCTCCCTC 2840
 TCGGCTGTGCCTTACGGAGCCCCAATCCAGGCCTCCTGTG 2880
 GCTGTTGGGTTCCAGATGCTGCAGCTCCATGTGACTTCCA 2920
 AGCAGGCCCTCCGCCCTCCCTGCTGAATGGAGGAGCCGGG 2960
 GGTCCCCCAGGCCAACTGGAAAATCTCCCAGGCTAGGCCA 3000
 3010 3020 3030 3040
 ATTGCCTTTTGCACCTTCCCCGTTCTGTACATTTCCCCA 3040
 GCCCCACCTTCCCCCTCCTGATGCCCTGAAAGCTTCCGGAA 3080
 TTGACTGTGACCACTTGGATGTCACCACTGTCAGCCCCTG 3120
 CCTTGATGTCCCCATTTAGCCATCTCCATGGAGCTCCTGC 3160
 TGGAGGGCCCTGAACCCTGCACTGCGTGGCTGCCCAGCCA 3200
 3210 3220 3230 3240
 GCTGCCTCCTGTCTCTGGGAGGAGGCCTCCTGGGTGTCCTC 3240
 ATCTGGTGTGTCTACTGGAGGGTCCCACAGGAGAGGCAGC 3280
 AGAGGGGTCAGGGGAGGTCTCCTGCCGGGGGTTGGCCTCT 3320
 CAAGCCTCAGGGGTTCTAGCCTGTTGAATATACCCACCT 3360
 GGTGGGTGGCCCCCTCCGATGTCCCCACTGATGGCTCTGAC 3400
 3410 3420 3430 3440
 ACCGTGTTGGTGGCGATGTCCCAGACAATCCCACCAGGAC 3440
 GGCCCAGACATCCCTACTGGCTTCGCTGGTGGCTCATCTC 3480
 GAACATCCACGCCAGCCTTTCTGGGGCCGGCCACCCAGGC 3520
 CGCCTGTCCGTCTGTCTCCTCCCTCCAGCAGCACCCCTGGC 3560
 CCCTGGAGTGGTGGGGCCATGGCAAGAGACACCGTGGCGT 3600
 3610 3620 3630 3640
 CTCATGTGAACCTTTCTGGGCACTGTGGTTTTATTTCTTA 3640
 ATTGATTTAAGAAATAAACCTGAAGACCGTCTGGTGAAAA 3680
 AAAAAAAAAAAAAA 3694

Fig. 44C

0940550460

hsFATP1 full lenght.protein

10 20 30 40
 MRAPGAGAASVVSALLWLLGLPWTWSAAAALGVYVGSGG 40
 WRFLRIVCKTARRDLFGLSVLIRVRLELRRHORAGHTIPR 80
 IFQAVVQRQPERLALVDAGTGECWTFAQLDAYSNVANLF 120
 RQLGFAPGDVVAIFLEGRPEFVGLWLGLAKAGMEAALLNV 160
 NLRREPLAFCLGTSGAKALIFGGEMVAAVA EVSGHLGKSL 200
 210 220 230 240
 IKFCSGDLGPEGILPDTHLLDPLLKEASTAPLAQIPSKGM 240
 DDRLFYIYTS GTTGLPKAAIVVHSRYRMAAFGHHAYRMQ 280
 AADVLYDCLPLYHSAGNIIGVGQCL IYGLTVVLRKKFSAS 320
 RFWDDCIKYNCTVVQYIGEICRYLLKQPVREAERRHRVRL 360
 AVGNGLRPAIWEEFTERFGVRQIGEFYGATECNC SIANMD 400
 410 420 430 440
 GKYGSCGFNSRILPHVYPIRLVKVNEDTMELLRDAQGLCI 440
 PCQAGEPGLLVGQINQQDPLRRFDGYVSESATSKKIAHSV 480
 FSKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVS 520
 TTEVEGVLSRLLGQTDVAVYGVAVPGVEGKAGMAAVAOPH 560
 SLLDPNAIYQELQKVLAPYARPIFLRLLPQVDTTGTFKIQ 600
 610 620 630 640
 KTRLQREGFDPRQTS DRLFFLDLKQGHYLP LNEAVYTRIC 640
 SGAFAL. 647

Fig. 45

hsVLACS full lenght.DNA

10 20 30 40
 GGAATTCCAAAAAAAAAATACGACTACACCTGCTCCGG 40
 AGCCCGCGGCGGTACCTGCAGCGGAGGAGCTCTGTCTTCC 80
 CCTTCATCTCACGCGAGCCCGGCGTCCCGCCGCGTGCGCC 120
 CCGGCGCAGCCCGCCAGTCCGCCCGGAGCCCGCCAGTCG 160
 CCGCGCTGCACGCCCGGGGTGAACCCTCTGCCCTCGCTGG 200

210 220 230 240
 GACAGAGGGCCCCGCGAGCCGTCATGCTTTCCGCCATCTAC 240
 ACAGTCCTGGCGGGACTGCTGTTCTGCGCTCCTGGTGA 280
 ACCTCTGCTGCCCATACTTCTTCCAGGACATAGGCTACTT 320
 CTTGAAGGTGGCCGCCGTGGGCCGGAGGGTGCGCAGCTAC 360
 GGGCAGCGGCGGCCGGCGCGCACCATCCTGCGGGCGTTCC 400

410 420 430 440
 TGGAGAAAGCGCGCCAGACGCCACACAAGCCTTTTCTGCT 440
 CTTCCGCGACGAGACTCTCACCTACGCGCAGGTGGACCGG 480
 CGCAGCAATCAAGTGGCCCCGGGCGCTGCACGACCACCTCG 520
 GCCTGCGCCAGGGAGACTGCGTGGCGCTCCTTATGGGTAA 560
 CGAGCCGGCCTACGTGTGGCTGTGGCTGGGGCTGGTGAAG 600

610 620 630 640
 CTGGGCTGTGCCATGGCGTGCCTCAATTACAACATCCGCG 640
 CGAAGTCCCTGCTGCACTGCTTCCAGTGCTGCGGGGCGAA 680
 GGTGCTGCTGGTGTGCGCCAGAACTACAAGCAGCTGTGCGAA 720
 GAGATACTGCCAAGCCTTAAAAAAGATGATGTGTCCATCT 760
 ATTATGTGAGCAGAACTTCTAACACAGATGGGATTGACTC 800

810 820 830 840
 TTTCCTGGACAAAGTGGATGAAGTATCAACTGAACCTATC 840
 CCAGAGTCATGGAGGTCTGAAGTCACTTTTCCACTCCTG 880
 CTTATACATTTATACTTCTGGAACCACAGGTCTTCCAAA 920
 AGCAGCCATGATCACTCATCAGCGCATATGGTATGGAAC 960
 GGCTCACTTTTGTAAGCGGATTGAAGGCAGATGATGTCA 1000

1010 1020 1030 1040
 TCTATATCACTCTGCCCTTTTACCACAGTGCTGCACTACT 1040
 GATTGGCATTACGGATGTATTGTGGCTGGTGCTACTCTT 1080
 GCCTTGCGGACTAAATTTTCAGCCAGCCAGTTTGGGATG 1120
 ACTGCAGAAAAATAACGTCACTGTCATTCACTATATCGG 1160
 TGAAGTGCCTTCGGTATTTATGCAACTCACCACAGAAACCA 1200

Fig. 46 A

66260"40550460

hsVLACS full lenght.DNA

1210 1220 1230 1240
 AATGACCGTGATCATAAAGTGAGACTGGCACTGGGAAATG 1240
 GCTTACGAGGAGATGTGTGGAGACAATTTGTCAAGAGATT 1280
 TGGGGACATATGCATCTATGAGTTCTATGCTGCCACTGAA 1320
 GGCAATATTGGATTTATGAATTATGCGAGAAAAGTTGGTG 1360
 CTGTTGGAAGAGTAAACTACCTACAGAAAAAATCATAAC 1400

1410 1420 1430 1440
 TTATGACCTGATTAAATATGATGTGGAGAAAGATGAACCT 1440
 GTCCGAGATGAAAATGGATATTGCGTCAGAGTTCCCAAAG 1480
 GTGAAGTTGGACTTCTGGTTTGCAAAATCACACAACCTTAC 1520
 ACCATTTAATGGCTATGCTGGAGCAAAGGCTCAGACAGAG 1560
 AAGAAAAAAGTGAAGATGTCTTTAAGAAAGGAGACCTCT 1600

1610 1620 1630 1640
 ATTTCAACAGTGGAGATCTCTTAATGGTTGACCATGAAAA 1640
 TTTTCATCTATTTCCACGACAGAGTTGGAGATACATTCCGG 1680
 TGGAAAGGGGAAAATGTGGCCACCACTGAAGTTGCTGATA 1720
 CAGTTGGACTGGTTGATTTTGTCCAAGAAGTAAATGTTTA 1760
 TGGAGTGCATGTGCCAGATCATGAGGGTCGCATTGGCATG 1800

1810 1820 1830 1840
 GCCTCCATCAAAATGAAAGAAAACCATGAATTTGATGGAA 1840
 AGAAACTCTTTTCAGCACATTGCTGATTACCTACCTAGTTA 1880
 TGCAAGGCCCGGTTTCTAAGAATACAGGACACCATTGAG 1920
 ATCACTGGAACTTTTAAACACCGCAAAATGACCCTGGTGG 1960
 AGGAGGGCTTTAACCCTGCTGTCATCAAAGATGCCTTGTA 2000

2010 2020 2030 2040
 TTTCTTGGATGACACAGCAAAAATGTATGTGCCTATGACT 2040
 GAGGACATCTATAATGCCATAAGTGCTAAAACCTGAAAC 2080
 TCTGAATATTCCCAGGAGGATAACTCAACATTTCCAGAAA 2120
 GAAACTGAATGGACAGCCACTTGATATAATCCAACCTTAA 2160
 TTTGATTGAAGATTGTGAGGAAATTTGTAGGAAATTTGC 2200

2210 2220 2230 2240
 ATACCCGTAAAGGGAGACTTTTTTAAATAACAGTTGAGTC 2240
 TTTGCAAGTAAAAAGATTTAGAGATTATTATTTTTCAGTG 2280
 TGCACCTACTGTTTGTATTTGCAAACTGAGCTTGTGGAG 2320
 GGAAGGCATTATTTTTTAAATACTTAGTAAATTAAATGA 2360
 AC 2362

Fig. 4bB

66260"4050460

hsVLACS full lenght.protein

10 20 30 40
 MLSAIYTVLAGLLFLPLLVLNCCPYFFQDIGYFLKVAAVG 40
 RRVRSYGQRRPARTILRAFLEKARQTPHKPFLFRDETLT 80
 YAQVDRRSNQVARALHDHLGLRQGDCVALLMGNEPAYVWL 120
 WLGLVKLGCAMACLNYNIRAKSLLHCFQCCGAKVLLVSPE 160
 LQAAVEEILPSLKKDDVSIYYVSRTSNTDGDIDFSLDKVDE 200
 210 220 230 240
 VSTEPIPESWRSEVTFSTPALYIYTS GTTGLPKAAMITHQ 240
 RIWYGTGLTFVSGLKADDVIYITLPFYHSAALLIGIHGCI 280
 VAGATLALRTKFSASQFWDDCRKYNVTVIQYIGELLRYLC 320
 NSPQKPNDRDHKVRLALGNGLRGDVWRQFVKRFGDICIYE 360
 FYAATEGNIGFMNYARKVGAVGRVNYLQKKIITYDLIKYD 400
 410 420 430 440
 VEKDEPVRDENGVCVRVPKGEVGLLVCKITQLTPFNGYAG 440
 AKAQTEKKKLRDVFKKGDLYFNSGDLLMVDHENFIYFHDR 480
 VGDTRFWKGENVATTEVAOTVGLVDFVQEVNVYGVHVPDH 520
 EGRIGMASIKMKENHEFDGKKLFQHIADYLPYARPRFLR 560
 IQDTIEITGTGFKHRKMTLVEEGFNPAVIKOALYFLDDTAK 600
 610 620 630 640
 MYVPMTEIYNAISAKTLKL. 621

Fig. 47

662260"40550460

hsFATP3 partial.DNA

10 20 30 40
AAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGC 40
ACAGGGTGACGGTGTTCCAGTACATTGGGGAGCTGTGCCG 80
ATACCTTGTCACCAGCCCCGAGCAAGGCAGAACGTGGC 120
CATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAG 160
ATACCTGGGAGCGTTTTGTGCGGCGCTTCGGGCCCCTGCA 200

210 220 230 240
GGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCC 240
ACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTG 280
CTTCCTGGCTTTACAAGCATATCTTCCCCTTCTCCTTGAT 320
TCGCTATGATGTCACCACAGGAGAGCCAATTGCGGACCCC 360
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGC 400

410 420 430 440
TGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCATTCTGGG 440
CTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTA 480
AAGGATGTCTCCGGCCTGGGGATGTTTTCTTCAACACTG 520
GGGACCTGCTGGTCTGCGATGACCAAGGTTTTCTCCGCTT 560
CCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAG 600

610 620 630 640
AATGTGGCCACAACCGAGGTGGCAGAGGTCTTCGAGGCC 640
TAGATTTTCTTCAGGAGGTGAACGTCTATGGAGTCACTGT 680
GCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTT 720
CTGCGTCCCCCCCACGCTTTGGACCTTATGCAGCTCTACA 760
CCCACGTGTCTGAGAACTTGCCACCTTATGCCCGGCCCCG 800

810 820 830 840
ATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACC 840
TTCAAACAGCAGAAAGTTCGGATGGCAAATGAGGGCTTCG 880
ACCCAGCACCCCTGTCTGACCCACTGTACGTTCTGGACCA 920
GGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTAC 960
AGCGCCCTCCTGGCAGGAAACCTTCGAATCTGAGAACTTC 1000

1010 1020 1030 1040
CACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGG 1040
GGCCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTA 1080
TACCAGAACTGCGGTCACTATTTTGTAATAAATGTGGCTG 1120
GAGCTGATCCAGCTGTCTCTGACAAAAAAAAAAAAAAAAAA 1160
AAAGGGCGGCCGC 1173

Fig. 48

005504-09260-66

hsFATP3partial.protein

...

10 20 30 40

KFSAGQFWEDCQOHRVTVFQYIGELCRYLVNQPPSKAERG 40
 HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVA 80
 TINYTGQRGAVGRASWLYKHIFPFLIRYDVTGEPIDP 120
 QGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQKLL 160
 KDVFRPGDVFFNTGDLLVCDDQGFLRFHVRTGDTFRWKGE 200

210 220 230 240

NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALV 240
 LRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTET 280
 FKQKKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARY 320
 SALLAGNLRI. 331

Fig. 49

66E260" 40550460

hsFATP4 full length

1

10 20 30 40

CGACCCACGCGTCCGGGCGGGCGGGGCCGGGCGGCGGGCG 40
 GGGCTGGCGGGGCGGGCCATGCAGGGCGCAGAGCCG 80
 GCTAAACCCTGCTGAGACCCGGCTCCGTGCGTCCAGGGGC 120
 GGCTAATGCCCTCACGCTGTCTACGCTGCTGCAACCGGG 160
 CCGCATCTGGACGGGCGCGCGGGCGGAGCCGACGCCG 200

210 220 230 240

GGCCACAATGCTGCTTGGAGCCTCTCTGGTGGGGGTGCTG 240
 CTGTTCTCCAAGCTGGTGTGAAACTGCCCTGGACCCAGG 280
 TGGGATTCTCCCTGTTGTTCTCTACTTGGGATCTGGCGG 320
 CTGGCGCTTCATCCGGGTCTTCATCAAGACCATCAGGCGC 360
 GATATCTTTGGCGGCCTGGTCCTCCTGAAGGTGAAGGCAA 400

410 420 430 440

AGGTGCGACAGTGCCTGCAGGAGCGGGCGGACAGTGCCCAT 440
 TTTGTTTGCCTCTACCGTTCGGCGCCACCCCGACAAGACG 480
 GCCCTGATCTTCGAGGGCACAGATAACCACTGGACCTTCC 520
 GCCAGCTGGATGAGTACTCAAGCAGTGTAGCCAACTTCCT 560
 GCAGGCCCCGGGCGCTGGCCTCGGGCGATGTGGCTGCCATC 600

610 620 630 640

TTCATGGAGAACCGCAATGAGTTCGTGGGCCTATGGCTGG 640
 GCATGGCCAAGCTCGGTGTGGAGGCAGCCCTCATCAACAC 680
 CAACCTGCGGCGGGATGCTCTGCTCCACTGCCTCACCACC 720
 TCGCGCGCACGGGCCCTTGTCTTTGGCAGCGAAATGGCCT 760
 CAGCCATCTGTGAGGTCCATGCCAGCCTGGACCCCTCGCT 800

810 820 830 840

CAGCCTCTTCTGCTCTGGCTCCTGGGAGCCCGGTGCGGTG 840
 CCTCCAAGCACAGAACACCTGGACCCTCTGCTGAAAGATG 880
 CTCCCAAGCACCTTCCAGTTGCCCTGACAAGGGCTTCAC 920
 AGATAAACTGTTCTACATCTACACATCCGGCACCACAGGG 960
 CTGCCCCAAGGCCGCCATCGTGGTGCACAGCAGGTATTACC 1000

1010 1020 1030 1040

GCATGGCTGCCCTGGTGTACTATGGATTCCGCATGCGGCC 1040
 CAACGACATCGTCTATGACTGCCTCCCCCTCTACCACTCA 1080
 GCAGGAAACATCGTGGGAATCGGCCAGTGCCTGCTGCATG 1120
 GCATGACGGTGGTGAATCGGAAGAAGTTCTCAGCCTCCCG 1160
 GTTCTGGGACGATTGTATCAAGTACAAGTGCACGATTGTG 1200

Fig. 50A

66260-10550460

hsFATP4 full length

1210 1220 1230 1240
 CAGTACATTGGTGAAGTGTGCCGCTACCTCCTGAACCAGC 1240
 CACCGCGGGAGGCAGAAAACCAGCACCAGGTTGCGATGGC 1280
 ACTAGGCAATGGCCTCCGGCAGTCCATCTGGACCAACTTT 1320
 TCCAGCCGCTTCCACATACCCAGGTGGCTGAGTTCTACG 1360
 GGGCCACAGAGTGCAACTGTAGCCTGGGCAACTTCGACAG 1400

1410 1420 1430 1440
 CCAGGTGGGGGCTGTGGTTTCAATAGCCGCATCCTGTCC 1440
 TTCGTGTACCCCATCCGGTTGGTACGTGTCAACGAGGACA 1480
 CCATGGAGCTGATCCGGGGGGCCGACGGCGTCTGCATTCC 1520
 CTGCCAGCCAGGTGAGCCGGGCCAGCTGGTGGGCCGCATC 1560
 ATCCAGAAAGACCCCTGCGCCGCTTCGATGGCTACCTCA 1600

1610 1620 1630 1640
 ACCAGGGCGCCAACAACAAGAAGATTGCCAAGGATGTCTT 1640
 CAAGAAGGGGGACCAAGGCCTACCTTACTGGTGATGTGCTG 1680
 GTGATGGACGAGCTGGGCTACCTGTACTTCCGAGACCGCA 1720
 CTGGGGACACGTTCCGCTGGAAAGGTGAGAACGTGTCCAC 1760
 CACCGAGGTGGAAGGCACACTCAGCCGCCTGCTGGACATG 1800

1810 1820 1830 1840
 GCTGACGTGGCCGTGTATGGTGTGCGAGGTGCCAGGAACCG 1840
 AGGGCCGGGGCCGAATGGCTGCTGTGGCCAGCCCCACTGG 1880
 CAACTGTGACCTGGAGCGCTTTGCTCAGGTCTTGGAGAAG 1920
 GAACTGCCCCCTGTATGCGCGCCCCATCTTCTGCGCCTCC 1960
 TGCCTGAGCTGCACAAAACAGGAACCTACAAGTTCCAGAA 2000

2010 2020 2030 2040
 GACAGAGCTACGGAAGGAGGGCTTTGACCCGGCTATTGTG 2040
 AAAGACCCGCTGTTCTATCTAGATGCCCAGAAGGGCCGCT 2080
 ACGTCCCGCTGGACCAAGAGGCCTACAGCCGCATCCAGGC 2120
 AGGCGAGGAGAAGCTGTGATTCCCCCATCCCTCTGAGGG 2160
 CCGGCGGATGCTGGATCCGGAGCCCCAGGTTCCGCCCCAG 2200

2210 2220 2230 2240
 AGCGGTCCTGGACAAGGCCAGACCAAGCAAGCAGGGCCT 2240
 GGCACCTCCATCCTGAGGTGCTGCCCCCTCCATCCAAACT 2280
 GCCAAGTGACTCATTGCCTTCCCAACCCTTCCAGAGGCTT 2320
 TCTGTGAAAGTCTCATGTCCAAGTTCCGTCTTCTGGGCTG 2360
 GGCAGGCCCTCTGGTTCCAGGCTGAGACTGACGGGTTTT 2400

2410 2420 2430 2440
 CTCAGGATGATGTCTTGGGTGAGGGTAGGGAGAGGACAAG 2440
 GGGTCACCGAGCCCTTCCCAGAGAGCAGGGAGCTTATAAA 2480
 TGGAACCAGAGCAGAAGTCCCCAGACTCAGGAAGTCAACA 2520
 GAGTGGGCAGGGACAGTGGTAGCATCCATCTGGTGGCCAA 2560
 AGAGAATCGTAGCCCCAGAGCTGCCCAAGTTCACTGGGCT 2600

Fig. 50B

66260" 10550460

2610 2620 2630 2640

CCACCCCCACCTCCAGGAGGGGAGGAGAGGACCTGACATC 2640
TGTAGGTGGCCCCCTGATGCCCATCTACAGCAGGAGGTCA 2680
GGACCACGCCCTTGGCCTCTCCCCACTCCCCCATCCTCCT 2720
CCCTGGGTGGCTGCCTGATTATCCCTCAGGCAGGGCCTCT 2760
CAGTCCTTGTGGGTCTGTGTCACCTCCATCTCAGTCTTGG 2800

2810 2820 2830 2840

CCTGGCTATGAGGGGAGGAGGAATGGGAGAGGGGGCTCAG 2840
GGGCCAATAAACTCTGCCTTGAGTCCTCCTAAAAAAAAAA 2880
AA 2907

Fig. 50C

03/01/2014 12:04 PM

hsFATP4 full length. protein

66E260"40550460

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      10      20      30      40
MLLGASLVGVLLFSKLVLPWTQVGFSLFLYLGGGWR 40
FIRVFIKTIRRDIFGGLVLLKVKAKVRQCLQERRTPILF 80
ASTVRRHPDKTALIFEGTDTHWTFRQLDEYSSSVANFLQA 120
RGLASGDVAAIFMENRNEFVGLWLGMAKLGVEAALINTNL 160
RRDALLHCLTTSRARALVFGSEMASAICEVHASLDPSLSL 200
      210      220      230      240
FCSGSWEPEGAVPPSTEHLDPDLLKDAPKHLPSCPDKGFTDK 240
LFYIYTSGTTGLPKAAIVVHSRYRMAALVYYGFRMRPND 280
IVYDCLPLYHSAGNIVGIGQCLLHGMTVVIRKKFSASRFW 320
DDCIKYNCTIVQYIGELCRYLLNQPPREAENQHQVRMALG 360
NGLRQSIWTFSSRFHIPQVAEFYGATECNCNCSLGNFDSQV 400
      410      420      430      440
GACGFNSRILSFVYPIRLVRVNEDTMELIRGPDGVCIPCQ 440
PGEFGQLVGRIIQKDPLRRFDGYLNQGANNKKIAKDVFKK 480
GDQAYLTGQVLVMDDELGYLYFRDRTGDTFRWKGENVSTTE 520
VEGTLRLLDMADVAVYGVEVPGTEGRAGMAAVASPTGNC 560
DLERFAQVLEKELPLYARPIFLRLLPELHKTGTYSKFKTE 600
      610      620      630      640
LRKEGFDPAIVKQPLFYLDAQKGRYVPLDQEAYSRIQAGE 640
EKL 643

```

Fig. 51

>hsFATP5(partial)

GTCGTTGGGATCCTCGGCTGCTTAGATCTCGGAGCCACCTGTGTTCTGGCCCCCAAG
TTCTCTACTTCCTGCTTCTGGGA
TGACTGTCGGCAGCATGGCGTGACAGTGATCCTGTATGTGGGCGAGCTCCTGCGATA
CTTGTGTAACATTCCCCAGCAAC
CAGAGGACCGGACACATACAGTCCGCCTGGCAATGGGCAATGGACTACGGGCTGAT
GTGTGGGGAGACCTTCCAGCAGCG
TTTCGGTCCTATTTTCGGATCTNGGGAAGTCTTACGGGCTTCCACAGAAGGGCAACAT
GGGGCTTTAGTTCAAATATTGTT
GGGGGCGCTGCGGGGCCCTGGGGGCAAAGATGGAGCTTGCCTCCTCCGAATGCTGT
CCCCCTTTGAGCTGGTGCA GTTCG
ACATGGAGGCGGCGGAGCCTGTGAGGGACAATCAGGGCTTCTGCATCCCTGTAGGG
CTAGGGGAGCCGGGGCTGCTGTTG
ACCAAGGTGGTAAGCCAGCAACCCTTCGTGGGCTACCGCGGCCCCCGAGAGCTGTC
GGAACGGAAGCTGGTGCGCAACGT
GCGGCAATCGGGCGACGTTTACTACAACACCGGGGACGTACTGGCCATGGACCGCG
AAGGCTTCCTCTACTTCCGCGACC
GACTCGGGGACACCTTCCGATGGAAGGGCGAGAACGTGTCCACGCACGAGGTGGAG
GGCGTGTTGTCGCAGGTGGACTTC
TTGCAACAGGTTAACGTGTATGGCGTGTGCGTGCCAGGTTGTGAGGGTAAGGTGGGC
ATGGCTGCTGTGGCATTAGCCCC
CGGCCAGACTTTCGACGGGGAGAAAGTTGTACCAGCACGTTTCGCGCTTGGCTCCCTGC
CTACGCTACCCCCCATTTTCATCC
GCATCCAGGACGCCATGGAGGTCACCAGCACGTTCAAACCTGATGAAGACCCGGTTG
GTGCGTGAGGGCTTCAATGTGGGG
ATCGTGGTTGACCCTCTGTTTGTACTGGACAACCGGGGCCAGTCCTTCCGGCCCCCTG
ACGGCAGAAATGTACCAGGCTGT
GTGTGAGGGAACCTGGAGGCTCTGATCACCTGGCCAACCCACTGGGGTAGGGATCA
AAGCCAGCCACCCCCACCCCAACA
CACTCGGTGTCCCTTTTCATCCTGGGCCTGTGTGAATCCCAGCCTGGCCATACCCTCA
ACCTCAGTGGGCTGGAAATGACA
GTGGGCCCTGTAGCAGTGGCAGAATAAACTCAGMTGYGTTACAGAAA

Fig. 52

hsFATP5partial.protein

10 20 30 40
VVGILGCLDLGATCVLAPKFSTSCFWDDCRQHGVTVILYV 40
GELLRYLCNIPQQPEDRTHTVRLAMGNGLRADVWGDLPAA 80
FRSYFGSXEVLRASLEGQHGALVQILLGALRGPGGKDGAC 120
LLRMLSPFELVQFDMEAAEPVRDNQGFCLPVGLGEPGLLL 160
TKVVSQQPFVGYRGPRELSEKLVNRVRSQGDVYYNTGDV 200
210 220 230 240
LAMDREGFLYFRDRLGDTFRWKGENVSTHEVEGVLSQVDF 240
LQQVNVYGVCPGCEGKVGMAAVALAPGQTFDGEKLYQHV 280
RAWLPAYATPHFIRIQDAMEVTSTFKLMKTRLVREGFNVG 320
IVVDPLFVLDNRAQSFRPLTAEMYQAVCEGTWRL 354

Fig. 53

09405504-092399

hsFATP6 full lenght.DNA

10 20 30 40
AACGGCAAGTAAGCGCAACGCAATTAATGTGAGTAGCTCA 40
CTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGG 80
CTCGTATGTTGTGTGGAATTGTGAGCGGATACCAATTTCA 120
CACAGGAACCAGCTATGACATGATTACGAATTTAATACGA 160
CTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGG 200
210 220 230 240
CACGAGGGGTGCTGAGCCCCTGCGCGGTTTCTGGTGCGTA 240
GAGACTGTAAATCGCTGCGCTTCTCAGTCATCATCATCCC 280
AGCTTTTCCCGGCTCGAATTCAGCCTCCAACCTCAAGCTCG 320
CGGGAAAGACTACCTGAGAGGAGAAAAGCTTCTGTCCCTG 360
GACCTTCTTCTGAGGGTGGAGTCGGAGGCTCCCTGCTTTC 400
410 420 430 440
CAGCCGCCCAGTGACCCAAGCTTAATCTTCAGCACCCTT 440
GGGGCGACCTTTTCGGTGCAAACCTACGATTCTGTTTCTC 480
AGGATTCTCCTCCCATCCCGCTTCGCCCCGGAAAAGCTGAC 520
AAGAACTTCAGGTGTAAGCCCTGAGTAGTGAGGATCTGCG 560
GTCTCCGTGGAGAGCTGTGCCTGGAAGAGAAGGACGCTGG 600
610 620 630 640
TGGGGGCTGAGATCAGAGCTGTCTTCTGGCCCAGTTGCC 640
CCATGCTTCTGTGCTAGGCTAACAGTTCTAGGGGCTGGAAT 680
GGTCGTCCTGCACTTCTTGCAAGAACTCCTGTTCCCTTAC 720
TTTTGGGATGACTTCTGGTTTCGTGTTGAAGGTGGTGCTCA 760
TTATAATTCCGGCTGAAGAAGTATGAAAAGAGAGGGGAGCT 800
810 820 830 840
GGTGAAGTGTGCTGGATAAATTCTTGAGTCATGCCAAAAGA 840
CAACCTCGGAAACCTTTTCATCATCTATGAGGGAGACATCT 880
ACACCTATCAGGATGTAGACAAAAGGAGCAGCAGAGTGGC 920
CCATGTCTTCTGAACCATTCCTCTCTGAAAAAGGGGGAC 960
ACGGTGGCTCTGCTGATGAGCAATGAGCCGGACTTCGTTT 1000
1010 1020 1030 1040
ACGTGTGGTTTCGGCCTCGCCAAGCTGGGCTGCGTGGTGGC 1040
CTTTCTCAACACCAACATTCGCTCCAACCTCCCTCCTGAAT 1080
TGCATCCGCGCCTGTGGGCCCAGAGCCCTAGTGGTGGGCG 1120
CAGATTTGCTTGAACGGTAGAAGAAATCCTTCCAAGCCT 1160
CTCAGAAAATATCAGTGTTTGGGGGATGAAAGATTCTGTT 1200

Fig. 54A

hsFATP6 full lenght.DNA

1210 1220 1230 1240
 CCACAAGGTGTAATTTCACTCAAAGAAAACTGAGCACCT 1240
 CACCTGATGAGCCCGTGCCACGCAGCCACCATGTTGTCTC 1280
 ACTCCTCAAGTCTACTTGTCTTTACATTTTACCTCTGGA 1320
 ACAACAGGTCTACCAAAAAGCAGCTGTGATTAGTCAGCTGC 1360
 AGGTTTTAAGGGGTTCTGCTGTCCTGTGGGCTTTTGTTG 1400

1410 1420 1430 1440
 TACTGCTCATGACATTGTTTATATAACCCTTCTCTGTAT 1440
 CATAGTTCAGCAGCTATCCTGGGAATTTCTGGATGTGTTG 1480
 AGTTGGGTGCCACTTGTGTGTTAAAGAAGAAATTTTCAGC 1520
 AAGCCAGTTTTGGAGTGACTGCAAGAAGTATGATGTGACT 1560
 GTGTTTCAGTATATTGGAGAACCTTTGTCGCTACCTTTGCA 1600

1610 1620 1630 1640
 AACAATCTAAGAGAGAAGGAGAAAAAGGATCATAAGGTGCG 1640
 TTTGGCAATTGGAAATGGCATACGGAGTGATGTATGGAGA 1680
 GAATTTTTAGACAGATTTGGAAATATAAAGGTGTGTGAAC 1720
 TTTATGCAGCTACCGAATCAAGCATATCTTTCATGAACATA 1760
 CACTGGGAGAATTGGAGCAATTGGGAGAACAAATTTGTTT 1800

1810 1820 1830 1840
 TACAAACTTCTTTCCACTTTTGACTTAATAAAGTATGACT 1840
 TTCAGAAAAGATGAACCCATGAGAAATGAGCAGGGTTGGTG 1880
 TATTCATGTGAAAAAAGGAGAACCTGGACTTCTCATTTCT 1920
 CGAGTGAATGCAAAAAATCCCTTCTTTGGCTATGCTGGGC 1960
 CTTATAAGCACACAAAAGACAAATTGCTTTGTGATGTTTT 2000

2010 2020 2030 2040
 TAAGAAGGGAGATGTTTACCTTAATACTGGAGACTTAATA 2040
 GTCCAGGATCAGGACAATTTCTTTATTTTTGGGACCGTA 2080
 CTGGAGACACTTTTACATGGAAAGGAGAAAAATGTCGCAAC 2120
 CACTGAGGTTGCTGATGTTATTGGAATGTTGGATTTTATA 2160
 CAGGAAGCAAACGTCTATGGTGTGGCTATATCAGGTTATG 2200

2210 2220 2230 2240
 AAGGAAGAGCAGGAATGGCTTCTATTATTTTAAAACCAAA 2240
 TACATCTTTAGATTTGGAAAAAGTTTATGAACAAGTTGTA 2280
 ACATTTCTACCAGCTTATGCTTGTCCACGATTTTAAAGAA 2320
 TTCAGGAAAAAATGGAAGCAACAGGAACATTCAAACCTATT 2360
 GAAGCATCAGTTGGTGGAAAGATGGATTTAATCCACTGAAA 2400

2410 2420 2430 2440
 ATTTCTGAACCACTTTACTTTCATGGATAACTTGAAAAAGT 2440
 CTTATGTTCTACTGACCAGGGAACCTTTATGATCAAATAAT 2480
 GTTAGGGGAAATAAACTTTAAGATTTTATATCTAGAAC 2520
 TTTCAATGCTTTCTTAGGAAGAGTGAGAGGGGGGTATAT 2560
 GATTCTTTATGAAATGGGGAAAGGGAGCTAACATTAATTA 2600

Fig. 54B

09405504.092399

hsFATP6 full lenght.DNA

2610 2620 2630 2640
TGCATGTACTATATTTCTTAATATGAGAGATAATTTTTT 2640
AATTGCATAAGAATTTTAATTTCTTTTAATTGATATAAAC 2680
ATTAGTTGATTATTCTTTTTATCTATTTGGAGATTCAGTG 2720
CATAACTAAGTATTTTCCTTAATACTAAAGATTTTAAATA 2760
ATAAATAGTGGCTAGCGGTTTGGACAATCACTAAAAATGT 2800
2810 2820 2830 2840
ACTTTCTAATAAGTAAAATTTCTAATTTTGAATAAAAGAT 2840
TAAATTTTACTGAAAAAAAAAAAAAAAAAAAAATTGGCG 2880
GCCGC 2885

Fig. 54C

66E260"40550460

hsFATP6 full lenght.protein

...

10	20	30	40
MLLSWLTVLGAGMVVLHFLQKLLFPYFWDDFWFLKVLI 40			
IIRLKKYEKRGELVTVLDKFLSHAKRQPRKPFIIYEGDIY 80			
TYQDVDRSSRVAVHFLNHSSLKKGDTVALLMSNEPDFVH 120			
VWFLAKLGCVVAFLNTNIRSNSLLNCIRACGPRALVGA 160			
DLLGTVEEILPSLSENISVWGMKDSVPQGVISLKEKLSTS 200			
210	220	230	240
PDEPVPRSHHVVSLLKSTCLYIFTSGTTGLPKAAVISQLQ 240			
VLRSAYLWAFGCTAHDIVYITLPLYHSSAAILGISGVE 280			
LGATCVLKKKFSASQFWSOCKKYDVTVFQYIGELCRYLCK 320			
QSKREGEKDHKVRLAIGNGIRSDVWREFLDRFGNIKVCCEL 360			
YAATESSISFMNYTGRIGAIGRTNLFYKLLSTFDLIKYDF 400			
410	420	430	440
QKDEPMRNEQGWCIHVKKGEPGLLISRVNAKNPFFGYAGP 440			
YKHTKDKLLCDVFKKGDVYLNTGDLIVQDQDNFLYFWDRT 480			
GDTFRWKGENVATTEVADVIGMLDFIQEANVYGVAISGYE 520			
GRAGMASIILKPNTSLDLEKVYEQVVTFLPAYACPRFLRI 560			
QEKMEATGTFKLLKHQLVEDGFNPLKISEPLYFMDNLKKS 600			
610	620	630	640
YVLLTRELYDQIMLGEIKL. 620			

Fig. 55

66E260"40550460

mFATP1 full length.DNA

1

10 20 30 40

AAGTTCCCACTCCAGACTTCTGCGAGAACCCGTGAGGAAG 40
 CAGCGAGAACCGGGGTTTGTCAAGCCAGAGAAGGATGCGG 80
 ACTCCGGGAGCAGGAACAGCCTCTGTGGCCTCATTGGGGC 120
 TGCTTTGGCTTCTGGGACTTCCGTGGACCTGGAGCGCGGC 160
 GGCGGCGTTTCGGTGTGTACGTGGGTAGCGGTGGCTGGCGA 200

210 220 230 240

TTTCTGCGTATCGTCTGCAAGACGGCGAGGCGAGACCTCT 240
 TTGGCCTCTCTGTTCTGATCCGCGTGGCGCTAGAGCTACG 280
 ACGACACCGGCGAGCAGGAGACGATCCCACGCATCTTC 320
 CAGGCCGTGGCCAGCGACAGCCGGAGCGCCTGGCGCTGG 360
 TAGATGCGAGTAGCGGTATCTGCTGGACCTTCGCACAGCT 400

410 420 430 440

AGACACCTACTCCAATGCTGTGGCCAATCTGTTCTCTCCAG 440
 CTGGGCTTTGCGCCAGGCGATGTGGTGGCTGTGTTCTTGG 480
 AAGGCCGGCCGAGTTCGTGGGACTGTGGCTGGGCCTGGC 520
 CAAGGCCGGTGTAGTGGCTGCGCTTCTCAATGTCAACCTG 560
 AGGCGGGAGCCCCCTTGCTTCTGCTTGGGCACATCAGCTG 600

610 620 630 640

CCAAGGCCCTCATTTATGGCGGGGAGATGGCAGCGGCGGT 640
 GGCGGAGGTGAGTGAGCAGCTGGGGAAGAGCCTGCTCAAG 680
 TTCTGCTCTGGAGATCTGGGGCCTGAGAGCGTCTGCTG 720
 ACACGCAGCTTCTGGACCCCATGCTTGCTGAGGCGCCAC 760
 CACACCCCTGGCACAGGCCCCAGGCAAGGGCATGGATGAT 800

810 820 830 840

CGGCTATTTTACATCTATACTTCTGGGACCACCGGACTTC 840
 CTAAGGCGGCCATTGTGGTGCACAGCAGGTACTACCGCAT 880
 CGCAGCCTTCGGCCACCATTCCTACAGCATGCGGGCCAA 920
 GATGTGCTCTATGACTGCCTACCTCTCTACCACTCAGCAG 960
 GGAACATCATGGGCGTGGGACAGTGTATCATCTACGGGTT 1000

1010 1020 1030 1040

AACGGTGGTACTGCGCAAGAAGTTCTCCGCCAGCCGCTTC 1040
 TGGGACGACTGTGTCAAAATATAATTGCACGGTAGTGAGT 1080
 ACATCGGTGAAATATGCCGCTACCTGCTAAGGCAGCCGGT 1120
 TCGCGATGTAGAGCGGCGGCACCGCGTGCAGCTGGCCGTG 1160
 GGTAACGGACTGCGGCCAGCCATCTGGGAGGAGTTACGC 1200

Fig. 56A

04550460

mFATP1 full length.DNA

1210	1220	1230	1240

AGGGTTTCGGTGTGCGACAGATTGGCGAGTTCTACGGCGC 1240			
CACCGAATGCAACTGCAGCATTGCCAACATGGACGGCAAG 1280			
GTCGGCTCCTGCGGCTTCAACAGCCGTATCCTCACGCATG 1320			
TGTÁCCCCATCCGTCTGGTCAAGGTCAACGAGGACACGAT 1360			
GGAGCCACTGAGGGACTCCCAAGGCCTCTGCATCCCGTGC 1400			
1410	1420	1430	1440

CAGCCCGGGGAACCTGGGCTTCTCGTGGGCCAGATCAACC 1440			
AGCAAGACCCTCTGCGGCGCTTCGATGGCTATGTTAGTGA 1480			
CAGCGCCACCAACAAGAAGATTGCCACAGCGTGTTCCGA 1520			
AAGGGGGACAGCGCCTACCTTTCAGGTGACGTGCTAGTGA 1560			
TGGACGAGCTGGGGTACATGTACTTCCGTGACCGCAGCGG 1600			
1610	1620	1630	1640

GGATACCTTCCGATGGCGCGGCGAGAACGTATCCACCACG 1640			
GAGGTGGAAGCCGTGCTGAGCCGCCTGTTGGGCCAGACGG 1680			
ACGTGGCTGTGTATGGAGTGGCTGTGCCAGGAGTGGAGGG 1720			
GAAAAGCGGCATGGCGGCCATTGCAGACCCCCACAACCAG 1760			
CTGGACCCCTAACTCAATGTACCAGGAATTGCAGAAGGTTC 1800			
1810	1820	1830	1840

TTGCATCCTATGCCCAGCCCATCTTCCTGCGTCTTCTGCC 1840			
CCAAGTGGATACAACAGGCACCTTCAAGATCCAGAAGACC 1880			
CGACTACAGCGTGAAGGCTTTGACCCCCGCCAGACCTCAG 1920			
ACCGGCTCTTCTTTCTAGACCTGAAACAGGGACGCTACCT 1960			
ACCCCTGGATGAGAGAGTCCATGCCCGCATCTGCGCAGGC 2000			
2010	2020	2030	2040

GACTTCTCACTCTGAGCCTGGTGAGTGGGATGGCCCTGGA 2040			
CTTGTGAGACCAGGGAGCCGGACACCCCTGTTCAAGTGTT 2080			
TCTCCTGCCTGGCCACGTGGCCAGCAGCACCTGTGGGTGC 2120			
AGGAAACTGGAACCTGAGTGGCCGGGTGTCCCTTTCCTAC 2160			
AACCACCATGCACACATCTAGCCTCTGCCTTGGTCTTTT 2200			
2210	2220	2230	2240

TCTCCATCTCTTTCTCCTCCGTGCCAGCAGGAGCCCCACAG 2240			
ACACATTGGCTGCTGTGTCTGCAGTGGGACCGGTGTCTA 2280			
GGGGTCCATGCTGCAGGCTGTGACCCGCACTGGTGCCAC 2320			
CTCCCTTCCCCATTGTGCCTTAGGTTCCCTCCACTGTGCGC 2360			
CGGTGAAGCAAGTGGGGACCCACATAGCTGTTGTCCCTGC 2400			
2410	2420	2430	2440

TGAGGGTTGGTAGCAAATGCACCCTCATGTCTAGCTGGGAG 2440			
ACACATGCAGTCTCCCACTGACCCCCAATCAACTGAAGAT 2480			
ACTGTTTTGTATTATTGTTTTGAGATAGGGTCTCACTGTG 2520			
GAGGCCAAGCTGGCCTCAGGCTCACCCTCTACTGCCTCC 2560			
GGGCACCAGCCTGCAGTTTGATGACATGTATGCACTATTG 2600			

Fig. 56B

04405504-0999

06405504 - 062999

Fig. 56c

mFATP1 full length.protein

10 20 30 40
 MRTPGAGTASVASLGLLWLLGLPWTWSAAAAFGVYVSGG 40
 WRFLRIVCKTARRDLFGLSVLIRVRLELRRHRRAGDTIPR 80
 IFQAVARQPERLALVDASSGICWTFAQLDTYSNAVANLF 120
 LQLGFAPGDVVAVFLEGRPEFVGLWLGLAKAGVVAALLNV 160
 NLRREPLAFCLGTSAAKALIYGGEMAAVAEVSEQLGKSL 200
 210 220 230 240
 LKFCSGDLGPESVLPDTQLLDPLAEAPTTPLAQAPGKGM 240
 DDRLFYIYTSGLTGLPKAAIVVHSRYRIAAGHHSYSMR 280
 ANDVLYDCLPLYHSAGNIMGVQCIYGLTVVLRKKFSAS 320
 RFWDDCVKYNCTVVQYIGEICRYLLRQPVRDVERRHRVRL 360
 AVGNGLRPAIWEEFTQGFVVRQIGEFYGATECNCSIANMD 400
 410 420 430 440
 GKVGSCGFNSRILTHVYPIRLVKVNEDTMEPLRDSQGLCI 440
 PCQPGEPGLLVGQINQQDPLRRFDGYVSDSATNKKIAHSV 480
 FRKGDSAYLSGDVLMDELGYMYFRDRSGDTFRWRGENVS 520
 TTEVEAVLSRLLGQTDVAVYGVAVPGVEGKSGMAAIADPH 560
 NQLDPNSMYQELQKVLASYAQPIFLRLLPQVDTTGTFKIQ 600
 610 620 630 640
 KTRLQREGFDPRQTSDRLEFFLDLKQGRYLPLDERVHARIC 640
 AGDFSL. 647

Fig. 57

0405504-09550460

mVLACS(FATP2)full length.DNA

1

10 20 30 40

GACACAGTACTGCCGATGTTGGACAGAGGATCGCTTAACA 40
 GAACGAAATCTCAAAACAAATTAACAGGACCCGGTTGCTT 80
 GATTTCCCAAATCAGAAAAGGCTCGAAATGTCTAGAGGGG 120
 CTGACTGATGCAGCGGTGACCCGGACTGGAGACAGTTGGA 160
 CGCGATCATCTCTGGTGCTTTTGTTCAACCTTGAAACCTT 200

210 220 230 240

CGCCACAGGAGACTTGCTGAGCAGAGAAGCAAACGTGGA 240
 GAAACAAAGAGAGATCTAGCGAAAAGCCTCTGGGACCAAG 280
 GAGGGGAGGTGGGACTCTGGGTTGGCGGTGGCACCTGCTG 320
 CCGGCTATTAATAATAGGGTCGCGATGCGTTTATAAGGTG 360
 TTTGATTAAACAAAGACTCTATGAGAGAAGAATAACTAGC 400

410 420 430 440

AACAGCCCCACGTCTGAGTCGTCGCCTCCGACCTTTTTCA 440
 ACGTGGGTTCTTTGGGCCGAGCGTCGTTTGCCGAGAACTA 480
 GATCTCACCTGACCCCAAGCTGACAAAGCGCTGTGG 520
 CATCCTGGGCCACCCAAGCTGACAAGGGCGCGCCCCCTGA 560
 GCACACGAGGTGCCCCACGAGGGGGAGGGACCCACAGCCG 600

610 620 630 640

TCCCGCCCGCACCGCGGTGTCCGCTGCGGGCACCTGCAGC 640
 CGAGCCGCCACCCGAGTCGCAGCGCGTCCGGCGGCCGAA 680
 CCGGTCGTCAGCTCGTCAGCACCTGCTCTGCTTCTCTCC 720
 CGCCCGCCGCGCGCTGCACGCCTCGAGCGCTCCCTCGGC 760
 CCGGGCGGGGACCGGGGACCCCGCAGCCACCGCCATGCTG 800

810 820 830 840

CCTGTGCTCTACACCGGCCTGGCGGGGCTGCTGCTGCTGC 840
 CTCTGCTGCTCACCTGCTGCTGCCCCCTACCTCCTCCAGGA 880
 CGTGCGGTTCTTCTGCAACTGGCCAACATGGCCCGGCAG 920
 GTGCGCAGCTACCGGCAGCGGCGACCCGTGCGCACCATCC 960
 TGCATGTCTTCTTGGAGCAAGCGCGCAAGACCCCGCACAA 1000

1010 1020 1030 1040

GCCCTTCCTGCTGTTTCGCGACGAGACGCTTACCTACGCC 1040
 CAGGTAGACCGGCGCAGCAACCAAGTAGCGGAGCGCTGC 1080
 ATGATCACCTGGGCTGCGGCAGGGGGATTGCGTGGCCCT 1120
 CTTATGGGCAATGAGCCGGCCTACGTGTGGCTCTGGCTG 1160
 GGACTGCTCAAACCTGGGCTGTCCCATGGCGTGCCCTCACT 1200

Fig. 58A

09405504-092399

mVLACS(FATP2)full length.DNA

1210	1220	1230	1240

ACAACATCCGTGCCAAGTCTCTGCTACACTGCTTTTCAAGTG	1240		
CTGCGGGGGCGAAGGTGCTGCTGGCCTCCCCAGAGCTACAC	1280		
GAAGCTGTCGAGGAGGTTCTTCCAACCCTGAAAAAGGAGG	1320		
GCGTGTCCGTCTTCTACGTAAGCAGAACTTCTAACACTAA	1360		
TGGCGTGGACACAGTACTGGACAAAGTAGACGGGGTGTCTG	1400		
1410	1420	1430	1440

GCGGACCCCATCCCGGAGTCGTGGAGGTCTGAAGTCACGT	1440		
TCACCACACCCGCAGTCTACATATATACTTCGGGCACCAC	1480		
AGGTCTTCCAAAGGCTGCAACCATTAAATCACCATCGCCTC	1520		
TGGTATGGGACCAGCCTTGCCCTGAGGTCCGGAATTAAGG	1560		
CTCATGACGTCTCTACACCACCATGCCCCCTGTACCACAG	1600		
1610	1620	1630	1640

CGCGGCGCTCATGATTGGCCTCCACGGATGCATTGTGGTT	1640		
GGGGCTACATTTGCTTTGCGGAGCAAATTTTCAGCCAGCC	1680		
AGTTTTGGGACGACTGCAGGAAATACAACGCCACTGTCAT	1720		
TCAGTACATCGGTGAACTGCTTCGGTACCTCTGCAACACG	1760		
CCCCAGAAACCAAATGACCGGGACCACAAAGTGAAAATAG	1800		
1810	1820	1830	1840

CACTAGGAAATGGCTTACGAGGAGATGTGTGGAGAGAGTT	1840		
CATCAAGAGATTTGGGGACATTCACATTTATGAGTTCTAC	1880		
GCTTCCACTGAAGGCAACATTGGATTTATGAACTATCCAA	1920		
GAAAAATCGGAGCTGTTGGAAGAGAAAATTACCTACAAAA	1960		
AAAAGTTGTAAGGCACGAGCTGATCAAGTATGACGTGGAG	2000		
2010	2020	2030	2040

AAGGATGAGCCTGTCCGTGATGCAAATGGATATTGCATCA	2040		
AAGTCCCCAAAGGAGAGGTTGGACTCTTGATTTGCAAAAT	2080		
CACAGAGCTCACACCATTTTTTTGGCTATGCTGGAGGAAAG	2120		
ACCCAGACAGAGAAGAAAAAGCTCAGAGATGTTTTTAAGA	2160		
AAGGAGACGTCTACTTCAACAGTGGCGATCTCCTGATGAT	2200		
2210	2220	2230	2240

CGACCGTGAAAAATTTTCATCTATTTTTCACGACAGAGTTGGA	2240		
GACACCTTCCGGTGGAAAGGAGAGAATGTAGCTACCACGG	2280		
AAGTCGCTGACATTGTGGGACTGGTAGATTTTGTGGAAGA	2320		
AGTGAATGTTTACGGTGTGCCCGTGCCAGGTGATGAAGGT	2360		
CGCATCGGGATGGCCTCGATCAAGATGAAAGAAAACTACG	2400		
2410	2420	2430	2440

AGTTCAATGGAAAGAACTCTTTTCAGCACATCTCGGAGTA	2440		
CCTGCCCAGTTACTCGAGGCCTCGGTTTCTGAGAATACAA	2480		
GATACCATTGAGATCACCGGGACTTTTAAACACCGCAAAG	2520		
TGACCTGATGGAAGAGGGCTTTAACCCCTCAGTCATCAA	2560		
AGATACCTTGTATTTTCATGGATGACACAGAAAAAACATAC	2600		

Fig. 58B

005504 10950460

09405504-09299

Fig. 58C

mVLACS(FATP2)full length.prot

10 20 30 40
MLPVLYTGLAGLLLLPLLLTCCCPYLLQDVRFLLQLANMA 40
RQVRSYRQRRPVRTILHVFLEQARKTPHKPFLLFRDETLT 80
YAQVDRRSNQVARALHDHLGLRQGDVALFMGNEPAYVWL 120
WLGLLKLGCPMACLNYNIRAKSLLHCFQCCGAKVLLASPE 160
LHEAVEEVLP TLKKEGVSVFYVSRTSNTNGVDTVLDKVDG 200
210 220 230 240
VSADPIPESWRSEVTFTTPAVYIYTS GTTGLPKAATINHH 240
RLWYGTSALALRSGIKAHDVIYTTMPLYHSAALMIGLHGCI 280
VVGATFALRSKFSASQFWDDCRKYNATVIQYIGELLRYLC 320
NTPQKPNDRDHKVKIALGNGLRGDVWREFIKRFGDIHIYE 360
FYASTEIGNIGFMNYPRKIGAVGRENYLQKKVVRHEL IKYD 400
410 420 430 440
VEKDEPV RDANGYCIKVPKGEVGLLICKITELTPFFGYAG 440
GKTQTEKKLRDVFKKGDVYFNSGOLL MIDRENFIYFHDR 480
VGDTFRWKGENVATTEVADI VGLVDFVEEVNVYGVVPGH 520
EGRIGMASIKMKENYEFNGKKLFQHI SEYLPYSRPRFLR 560
IQDTIEITGTFKHKRVTLMEEGFNPSVIKDTLYFMD DTEK 600
610 620 630 640
TYVPMTEDIYNAIIDKTLKL. 621

Fig. 59

1 10 20 30 40
 GATCAGCTCTTCTATATCTACACGTCGGGCACCACGGGGC 40
 TACCCAAAGCTGCCATTGTGGTGCACAGCAGGTATTACCG 80
 AATGGCTGCCCTGGTGTACTATGGATTCCGCATGCGGCCT 120
 GATGACATTGTCTATGACTGCCTCCCCCTCTACCACTCAG 160
 CAGGAAACATTGTGGGGATTGGCCAGTTCGTACTCCACGG 200
 210 220 230 240
 CATGACTGTGGTGATCCGGAAGAAGTTTTTCAGCCTCCCGG 240
 TTCTGGGATGACTGTATCAAGTACAAGTGCACAATTGTAC 280
 AGTACATTGGTGAGCTTTGCCGCTACCTCCTGAACCAGCC 320
 ACCCCGTGAGGCTGAGTCTCGGCACAAGGTGCGCATGGCA 360
 CTGGGCAACGGTCTCCGGCAGTCCATCTGGACCGACTTCT 400
 410 420 430 440
 CCAGCCGTTTCCACATTCCCAAGGTGGCCGAGTTCTACGG 440
 GGCCACCGAGTGCAACTGTAGCTTGGGCAACTTTGACAGC 480
 CAGGTGGGGGCTGTGGCTTCAATAGCCGCATCCTGTCTT 520
 TTGTGTACCCCATCCGCTTGGTACGAGTCAATGAGGATAC 560
 CATGGAAGTATCCGGGGACCCGATGGCGTCTGCATTCCC 600
 610 620 630 640
 TGTCACCCAGGCCAGCCAGGCCAGCTGGTGGGTGCGCATCA 640
 TCCAGCAGGACCCCTACGCCGTTTTGATGGCTACCTCAA 680
 CCAGGGTGCCAACAACAAGAAGATTGCTAGTGATGTCTTC 720
 AAGAAAGGGGACCAAGCCTACCTCACTGGTGACGTGCTGG 760
 TGATGGATGAGCTGGGCTACCTGTACTTCCGAGACCGCAC 800
 810 820 830 840
 AGGGGACACGTTCCGCTGGAAAGGGGAGAATGTGTCTACC 840
 ACTGAAGTGGAGGGCACACTCAGCCGCCTGCTTCAGATGG 880
 CAGATGTGGCTGTTTATGGTGTGAGGTGCCAGGAGCTGA 920
 GGGCCGAGCAGGAATGGCTGCTGTGGCAAGCCCCACTAGC 960
 AACTGTGACCTGGAGAGCTTTGCACAGACCTTGAAAAAGG 1000
 1010 1020 1030 1040
 AGCTGCCCCTGTACGCCCGCCCCATCTTCCTCCGCTTCTT 1040
 GCCTGAGCTGCACAAAACAGGAACCTTCAAGTTCCAGAAG 1080
 ACAGAGTTGCGGAAGGAGGGCTTTGACCCGTCTGTTGTGA 1120
 AAGACCCACTCTTCTATTTGGATGCCCCGACAGGCTGCTA 1160
 TGTGCACTGGACCAAGAGGCCTATACCCGCATCCAGGCA 1200

Fig. 60A

mFATP4 partial.DNA

1210 1220 1230 1240
GGCGAGGAGAAGCTGTGATTTCCCCCACATCCCTCTGAGG 1240
GCCAGAGGATGCTGGATTTCAGAGCCCCAGCTTCCACTCCA 1280
GAAGGGGTCTGGGCAAGGCCAGACCAAAGCTAGCAGGGCC 1320
CGCACCTTCACCCTAGGTGCTGATCCCCCT 1350

Fig. 60B

09405504-09239
55E260-10550460

mFATP4partial.DNA

10 20 30 40
 DQLFYIYTS GTTGLPKAAIVVHSRYRMAALVYYGFRMRP 40
 DDIVYDCLPLYHSAGNIVGIGQCVLHGMTVVIRKKFSASR 80
 FWDDCIKYNCTIVQYIGELCRYLLNQPPREAESRHKVRMA 120
 LGNGLRQSIWTD FSSRFHIPKVAEFYGATECNC SLGNFDS 160
 QVGACGFNSRILSFVYPIRLVRVNEDTMELIRGPDGVCIP 200
 210 220 230 240
 CQPGQPGQLVGRIIQDDPLRRFDGYLNQGANNKKIASDVF 240
 KKGDDQAYLTGDVLMDELGYLYFRDRTGDTFRWKGENVST 280
 TEVEGTLSRLLQMAADVAVYGVEVPGAEGRAGMAAVASPTS 320
 NCDLESFAQTLKKELPLYARPIFLRFLPELHKTGTFFKFK 360
 TELRKEGFDPSVVKDPLFYLDARTGCVYALDQEAAYTRIOA 400
 410 420 430 440
 GEEKL. 406

Fig. 61

00550460

mmFATP1 full length.DNA

1

10 20 30 40

ATGCGGGCTCCTGGAGCAGGAACAGCCTCTGTGGCCTCAC 40
TGGCGCTGCTTTGGTTTCTGGGACTTCCGTGGACCTGGAG 80
CGCGGCGGCGGCGTTCTGTGTGTACGTGGGTGGCGGCGGC 120
TGGCGCTTTCTGCGTATCGTCTGCAAGACGGCGAGGCGAG 160
ACCTCTTTGGCCTCTCTGTTCTGATTCTGTTCGGCTAGA 200

210 220 230 240

GCTGCGACGACACCGGCGAGCAGGAGACACGATCCCGTGC 240
ATCTTCCAGGCTGTGGCCCGGCGACAACCAGAGCGCCTGG 280
CACTGGTGGACGCCAGTAGTGGTATATGCTGGACCTTCGC 320
ACAGCTGGACACCTACTCCAATGCTGTAGCCAACCTGTTT 360
CGCCAGCTGGGCTTTGCACCAGGCGATGTGGTGGCTGTGT 400

410 420 430 440

TCCTGGAGGGCCGGCCGGAGTTCGTGGGACTGTGGCTGGG 440
CCTGGCCAAGGCCGGTGTGGTGGCTGCTCTTCTCAATGTC 480
AACCTGAGGCGGGAGCCCCCTGGCCTTCTGCCTGGGCACAT 520
CAGCTGCCAAGGCCCTCATTTATGGCGGGGAGATGGCAGC 560
GGCGGTGGCGGAGGTGAGCGAGCAGCTGGGGAAGAGCCTC 600

610 620 630 640

CTCAAGTTCTGCTCTGGAGATCTGGGGCCTGAGAGCATCC 640
TGCCTGACACGCAGCTCCTGGACCCCATGCTTGCTGAGGC 680
GCCCCACACCCCTGGCACAAGCCCCAGGCAAGGGCATG 720
GATGATCGGCTGTTTTACATCTATACTTCTGGGACCACCG 760
GGCTTCCTAAGGCTGCCATTGTGGTGCACAGCAGGTACTA 800

810 820 830 840

CCGCATTGCTGCCTTTGGCCACCATTCCTACAGCATGCGT 840
GCCGCCGATGTGCTCTATGACTGCCTGCCACTCTACCACT 880
CTGCAGGGAACATCATGGGTGTGGGGCAGTGCATCATCTA 920
CGGGTTGACGGTGGTACTGCGCAAGAAGTTCTCCGCCAGC 960
CGCTTCTGGGATGACTGTGTCAAGTACAATTGCACGGTAG 1000

1010 1020 1030 1040

TGGATGACATAGGTGAAATCTGCCGCTACCTGCTGAGGCA 1040
GCCGGTTCGCGACGTGGAGCAGCGACACCGCGTGCGCCTG 1080
GCCGTGGGTAATGGGCTGCGGCCAGCCATCTGGGAGGAGT 1120
TCACGCAGCGCTTCGGTGTGCCACAGATCGGCGAGTTCTA 1160
CGGCGCTACCGAGTGCAACTGCAGCATTGCCAACATGGAC 1200

Fig. 62A

09405504.092399

mmFATP1 full length.DNA

1210 1220 1230 1240
 GGCAAGGTCGGCTCCTGCGGCTTCAACAGCCGTATCCTCA 1240
 CGCATGTGTACCCCATCCGTCTGGTCAAGGTCAATGAGGA 1280
 CACGATGGAGCCACTGCGGGACTCCGAGGGCCTCTGCATC 1320
 CCGTGCCAGCCCCGGGAACCCGGCCTTCTCGTGGGCCAGA 1360
 TCAACCAGCAGGACCTCTGCGGCGTTTCGATGGTTATGT 1400

1410 1420 1430 1440
 TAGTGACAGTGCCACCAACAAGAAGATTGCCACAGCGTT 1440
 TTCCGAAAGGGCGATAGCGCCTACCTCTCAGGTGACGTGC 1480
 TAGTGATGGACGAGCTGGGCTACATGTATTTCCGTGACCG 1520
 CAGCGGGGACACCTTCCGCTGGCGCGGGGAGAACGTGTCC 1560
 ACCACGGAGGTGGAAGCCGTGCTGAGCCGCCTACTGGGCC 1600

1610 1620 1630 1640
 AGACGGACGTGGCTGTGTATGGGGTGGCTGTGCCAGGAGT 1640
 GGAGGGGAAAGCTGGCATGGCAGCCATCGCAGATCCCCAC 1680
 AGCCAGTTGGACCCTAACTCAATGTACCAGGAATTACAGA 1720
 AGGTTCTTGCATCCTATGCTCGGCCCATCTTCTGCGTCT 1760
 TCTGCCCCAGGTGGATACCACAGGCACCTTCAAGATCCAG 1800

1810 1820 1830 1840
 AAGACCCGGCTGCAGCGTGAAGGCTTTGACCCCCGTCAGA 1840
 CCTCAGACAGGCTCTTCTTTCTAGACCTGAAGTCCGGCAC 1880
 GAGGTATCTACCCCTGGATGAGAGAGTCCATGCCCGCATT 1920
 TGCGCAGGCGACTTCTCACTCTGAGCCTGGAGAGTGGGCT 1960
 GGGCCTGGACTCCTGAGACCTGGGAGCCTGACACCCCTCT 2000

2010 2020 2030 2040
 TCGGGTGCTTCTCCTGCCTGGCCACATGGACAGCAGCACC 2040
 TGTGAGAGTAGGAAAATGGAACCTGAGTGGCTGGGACCCC 2080
 TCTCCTACTTCCCCTATGCATCCATTTTGCTCTGCCTT 2120
 GATCTTTTTTCTCCATCTCTTTTCTCCCTACCCAGCAGGAG 2160
 CCCCACAAACACATGTTGGCTGCTGTGTCCTGCAGTTGGA 2200

2210 2220 2230 2240
 CCAGTGTCAGGGGTACAGGCTTCAGGCTGTGACCCACAC 2240
 TGGTACCCACCTCCCTTTTCTATTTTGCCTTAGGTTTCATC 2280
 CACGGTTCCTCTGTGGAGCAAGTGGGGGCCACATAGCTG 2320
 CTGTCCCTGCTGAGGGTTGGTAGCAATCACACCCCTCATGT 2360
 CAGCTGGGAGACACGCGCAGTCTCCCACTGACCCCCAATC 2400

2410 2420 2430 2440
 AACTGAAAATATTGTTTTGACTACTTTTTGTTTTTTTGT 2440
 TTTTTGTTTTTTTTTTTTTCGAGACAGAGTTTCTCTGTA 2480
 TAGCCCTGGCTGTCTTGGAACTCACTTTGTAGACCAGGCT 2520
 GGCCTCGAACTCAAAAATCCTCCTGACTCTGCCTCTGCTT 2560
 CCAAGTGCTGGGATTAAAGACGTGCGCCACCACCGCCTG 2600

Fig. 62B

66260" 40550460

04405 EOL 02099

Fig. 62C

mmFATP1 full length.protein

10 20 30 40
 MRAPGAGTASVASLALLWFLGLPWTWSAAAAFCVYVGGGG 40
 WRFLRIVCKTARRDLFGLSVLIRVRLELRRHRRAGDTIPC 80
 IFQAVARRQPERLALVDASSGICWTFAQLDTYSNAVANLF 120
 RQLGFAPGDVVAVFLEGRPEFVGLWLGLAKAGVVAALLNV 160
 NLRREPLAFCLGTSAAKALIYGGEMAAVAEVSEQLGKSL 200
 210 220 230 240
 LKFCSGDLGPESILPDTQLLDPMLAEAPTTPLAQAPGKGM 240
 DDRLFYIYTSGTTGLPKAAIVVHSRYRIRIAAFGHHSYSMR 280
 AADVLYDCLPLYHSAGNIMGVGCVIYGLTVVLRKKFSAS 320
 RFWDDCVKYNCTVVDDIGEICRYLLRQPVRDVEQRHRVRL 360
 AVGNGLRPAIWEFTQRFGVPQIGEFYGATECNCSIANMD 400
 410 420 430 440
 GKVGSCGFNSRILTHVYPIRLVKVNEDTMEPLRDSEGLCI 440
 PCQPGEPGLLVGQINQQDPLRRFDGYVSDSATNKKIAHSV 480
 FRKGDSAYLSGDVLVMDLGYMYFRDRSGDTFRWRGENVS 520
 TTEVEAVLSRLLGQTDVAVYGVAVPGVEGKAGMAAIADPH 560
 SQLDPNSMYQELQKVLASYARPIFLRLLPQVDTTGTFKIQ 600
 610 620 630 640
 KTRLQREGFOPRQTSDRFLFDLKSGETRYLPLDERVHARI 640
 CAGDFSL 647

Fig. 63

556250"40550460

mmFATP2 full length.DNA

10 20 30 40
 GGGCGGAGGCCGAGCCAGTCGCCAGCTCCTGCTCTGCTC 40
 CTCTCCCGCCTGCCGCCGCGCTGCACGCCTCGAGCACTCC 80
 CTCGGCCCCGGCGGGGACCGGGGACCCCGCAGCTACCGCC 120
 ATGCTGCCAGTGCTCTACACCGGCCTGGCGGGGCTGCTGC 160
 TGCTGCCTCTGCTGCTCACCTGCTGCTGCCCTACCTCCT 200

210 220 230 240
 CCAAGATGTGCGGTACTTCCTGCGGCTGGCCAACATGGCC 240
 CGGCGGGTGCGCAGCTACCGGCAGCGCGACCCGTGCGTA 280
 CCATCCTGCGGGCCTTCCTGGAACAAGCGCGCAAGACCCC 320
 ACACAAGCCCTTCCTGCTGTTCCGAGACGAGACGCTCACC 360
 TACGCCCAGGTGGACCGGCGCAGCAACCAAGTGGCGCGGG 400

410 420 430 440
 CGCTGCACGATCAACTGGGCCTACGACAGGGGGATTGCGT 440
 AGCCCTCTTCATGGGCAATGAGCCGGCCTACGTGTGGATC 480
 TGGCTGGGACTGCTCAAACCTGGGCTGTCCCATGGCGTGCC 520
 TCAACTACAACATTCGTGCCAAGTCTCTGCTGCACTGCTT 560
 TCAATGCTGCGGGGCGAAGGTGCTGCTGGCCTCCCCAGAT 600

610 620 630 640
 CTACAAGAAGCTGTGGAGGAGGTTCTTCCAACCCTGAAAA 640
 AGGATGCCGTGTCCGTCTTTTACGTAAGCAGAACTTCTAA 680
 CACAAATGGTGTGGACACAATACTGGACAAAGTAGACGGA 720
 GTGTGGCGGAACCCACCCCGGAGTCGTGGAGGTCTGAAG 760
 TCACTTTTACCACGCCAGCAGTATACATTTATACTTCGGG 800

810 820 830 840
 AACCACAGGTCTTCCAAAAAGCGGAACCATCAATCATCAT 840
 CGCCTAAGGTATGGGACAAGCCTTGCTATGTCGAGTGGGA 880
 ATCACGGCCAAGGATGTCATCTATACCAACAATGCCCCCTG 920
 TTCCAACAGTGCAACGCTCAAGATCGGCCTTCACGGATGC 960
 ATCCTGGGTTGGGGCTACTTTAACCTTGGCGGGGCAAATT 1000

1010 1020 1030 1040
 CTCAAGCAAGCCAATTTTGGGAACGACTGGCAGGAAATAC 1040
 AACGTCAACGGTCAATTCAGTACATTGGTGAAGTCTTCGG 1080
 TACCTGTGCAACACACCGCAGAAACCAAATGACCGGGACC 1120
 ACAAAGTGAAAAAAGCCCTGGGAAATGGCTTACGAGGAGA 1160
 TGTGTGGAGAGAGTTCATCAAGAGATTTGGGGACATCCAC 1200

Fig. 64A

0945504.09299

mmFATP2 full length.DNA

```

      1210      1220      1230      1240
      | | | | | | | | | | | | | | | |
GTGTATGAGTTCTACGCATCCACTGAAGGCAACATTGGAT 1240
TTGTGAAGTATCCAAGGAAAATCGGTGCTGTCGGGAGAGC 1280
AAACTACCTACAAAGAAAAGTTGCAAGGTATGAGCTGATC 1320
AAGTATGACGTGGAGAAGGACGAGCCGGTCCGTGACGCAA 1360
ATGATATTGCATCAAAGTCCCCAAAGGTGAGGTTGGACT 1400

      1410      1420      1430      1440
      | | | | | | | | | | | | | | | |
CTTGTTTTGCAAAATCACACAGCTCACACCATTTATTGGC 1440
TATGCTGGAGGAAAGACCCAGACAGAGAAGAAAAAACTCA 1480
GAGATGTCTTTAAGAAAGGCGACATCTACTTCAACAGCGG 1520
AGACCTCCTGATGATCGACCGTGAGAACTTCGTCTACTTT 1560
CACGACAGGGTTGGAGATACTTTCCGGTGGAAGGAGAGA 1600

      1610      1620      1630      1640
      | | | | | | | | | | | | | | | |
ACGTAGCTACCACAGAAGTCGCTGACATCGTGGGACTGGT 1640
AGATTTTGTGAAGAAGTGAATGTGTATGGCGTGCCTGTG 1680
CCAGGTCATGAGGGTCGAATTGGGATGGCCTCCCTCAAGA 1720
TCAAAGAAAACACGAGTTCAATGGAAAGAACTCTTTCA 1760
ACACATCGCGGAGTACCTGCCAGTTACGCGAGGCCTCGG 1800

      1810      1820      1830      1840
      | | | | | | | | | | | | | | | |
TTCCTGAGGATACAAGATACCATTGAGATCACTGGGACTT 1840
TTAAACACCGCAAAGTGACCCTGATGGAAGAGGGCTTCAA 1880
TCCCACAGTCATCAAAGATACCTTGTATTTTCATGGATGAT 1920
GCAGAGAAAACATTTGTGCCCATGACTGAGAACATTTATA 1960
ATGCCATAATTGATAAACTCTGAAGCTCTGAATATTCCC 2000

      2010      2020      2030      2040
      | | | | | | | | | | | | | | | |
TGGTGGTTTTAGCTCATGACATTTCCAGAAAGAACTCGAT 2040
AGACCTCGCAGAGCCACTTCATACGTAGAATCCAACTTTA 2080
ACTTGATTGAAGACTATAAGGTGCGATTTTATTTTATAGGA 2120
AATTATTCATTAAAGGATAGTTTTTTTTTTTTTTTTTAA 2160
TTACACCTGAACCTTTGCAAGTAAAAAGATTTAGAGACAA 2200

      2210      2220      2230      2240
      | | | | | | | | | | | | | | | |
TTATTTTTCAATGTGCACCTGCCATTTGTCCTTGCAAAC 2240
AAGCTTCTTGAGAGAGGGCCTTATTTTTTTTAAAGACATA 2280
ATAAACTATATTAACACTAAAAAAAAAAAAAAAAAAAAAA 2320
AAAAAAAAAAAAAAAAAAAAA 2338

```

Fig. 64B

65250"40550460

mmFATP2 full length.protein

...

10 20 30 40

MLPVLYTGLAGLLLLPLLLTCCCPYLLQDVRYFLRLANMA 40
 RRVRSYRQRRPVRTILRAFLEQARKTPHKPFLLFRDETLT 80
 YAQVDRRSNQVARALHDQLGLRQDCVALFMGNEPAYVWI 120
 WLGLLKLGCPCMACLNYNIRAKSLLHCFQCCGAKVLLASPD 160
 LQEAVEEVLP TLKKDAVS VFYVSRTSNTNGVD TILDKVDG 200

210 220 230 240

VSAEPTESWRSEVTFTTPAVYIYTS GTTGLPKSGTINHH 240
 RLRYGTSLAMSSGNHGQGCHLYQQCPCSNSATLKIGLHGC 280
 ILGWGYFNLGGANSQASQFWERLAGNTTSTVIOYIGELLR 320
 YLCNTPKPNDRDHKVKKALGNGLRGDVWREFIKRFGDIH 360
 VYEFYASTE GNIGFVNYPRKIGAVGRANYLQRKVARYELI 400

410 420 430 440

KYDVEKDEPVRDANGYCIKVPKGEVGLLVCKITQLTPFIG 440
 YAGGKTQTEKKKL RDVFKKGDIYFN SGDLLMIDREN FVYF 480
 HDRVGD TFRWKGENVATTEVADIVGLVDFVEEVN VYGV PV 520
 PGHEGRIGMASLKIKENYEFNGKKLFQHIAEYLPSYARPR 560
 FLRIQDTIEITGTFKHKRVTLMEEGFNPTVIKDTLYFMDD 600

610 620 630 640

AEKTFVPM TENIYNAIIDKTLKL. 624

Fig. 65

552250"10550460

mmFATP3 partial.DNA

10 20 30 40
GAAAGCTCTGAGAGCGGGTGCAGTCTGGCCTGGCGTCTCG 40
CGTACCTGGCCCGGGAGCAGCCGACACACACCTTCCTCAT 80
CCACGGCGCGCAGCGCTTTAGCTACGCGGAGGCTGAGCGC 120
GAGAGCAACCGGATTGCTCGCGCCTTTCTGCGCGCACGGG 160
GCTGGACCGGGGGCCGCCGAGGCTCGGGCAGGGGCAGCAC 200
210 220 230 240
TGAGGAAGGCGCACGCGTGGCGCCTCCGGCTGGAGATGCG 240
GCTGCTAGAGGGACGACCGCGCCCCCTCTGGCACCCGGGG 280
CGACCGTGGCGCTGCTCCTCCAGCGGGCCCGGATTTCT 320
TTGGATTTGGTTCCGACTGGCCAAAGCTGGCCTGCGCACG 360
GCCTTTGTGCCACCGCTTTACGCCGAGGACCCCTGCTGC 400
410 420 430 440
ACTGCCTCCGCAGCTGCGGTGCGAGTGCCTCGTGCTGGC 440
CACAGAGTTCCTGGAGTCCCTGGAGCCGGACCTGCCGGCC 480
TTGAGAGCCATGGGGCTCCACCTATGGGCGACGGGGCCCTG 520
AAACTAATGTAGCTGGAATCAGCAATTTGCTATCGGAAGC 560
AGCAGACCAAGTGGATGAGCCAGTGCCGGGGGTACCTCTCT 600
610 620 630 640
GCCCCCAGAACATAATGGACACCTGCCTGTACATCTTCA 640
CCTCTGGCACTACTGGCCTGCCCAAGGCTGCTCGAATCAG 680
TCATCTGAAGTTCTACAGTGCCAGGGATTCTACCATCTG 720
TGTGGAGTCCACCAGGAGGACGTGATCTACCTCGCACTCC 760
CACTGTACCACATGTCTGGCTCCCTTCTGGGCATTGTGGG 800
810 820 830 840
CTGCTTGGGCATTGGGGCCACCGTGGTGCTGAAACCCAAG 840
TTCTCAGCTAGCCAGTTCTGGGACGATTGCCAGAAACACA 880
GGGTGACAGTGTTCAGTACATTGGGGAGTTGTGCCGATA 920
CCTCGTCAACCAGCCCCCGAGCAAGGCAGAGTTTGACCAT 960
AAGGTGCGCTTGGCAGTGGGCAGTGGGTTCGCGCCAGACA 1000
1010 1020 1030 1040
CCTGGGAGCGTTTCTGCGGCGATTTGGACCTCTGCAGAT 1040
ACTGGAGACGTATGGCATGACAGAGGGCAACGTAGCTACG 1080
TTCAATTACACAGGACGGCAGGGTGCAGTGGGGCGAGCTT 1120
CCTGGCTTTACAAGCACATCTTCCCCTTCTCCTTGATTCTG 1160
ATACGATGTCATGACAGGGGAGCCTATTTCGGAATGCCAG 1200

Fig. 66A

66260"40550460

054035600 054035600

Fig. 66B

0940504-4090460

Fig. 67

mmFATP4 full length.DNA

10 20 30 40
 ATGCTGCTTGGAGCCTCTCTGGTGGGGGCGCTACTGTTCT 40
 CCAAGCTAGTGCTGAAGCTGCCCTGGACCCAGGTGGGATT 80
 CTCCCTGTTGCTCCTGTACTTGGGGTCTGGTGGCTGGCGT 120
 TTCATCCGGGTCTTTCATCAAGACGGTCAGGAGAGATATCT 160
 TTGGTGGCATGGTGCTCCTGAAGGTGAAGACCAAGGTGCG 200
 210 220 230 240
 ACGGTACCTTCAGGAGCGGAAGACGGTGCCCTGCTGTTT 240
 GCTTCAATGGTACAGCGCCACCCGGACAAGACAGCCCTGA 280
 TTTTCGAGGGCACAGACACTCACTGGACCTTCCGCCAGCT 320
 GGATGAGTACTCCAGTAGTGTGGCCAACCTCCTGCAGGCC 360
 CGGGGCCTGGCCTCAGGCAATGTAGTTGCCCTCTTTATGG 400
 410 420 430 440
 AAAACCGCAATGAGTTTGTGGGTCTGTGGCTAGGCATGGC 440
 CAAGCTGGGCGTGGAGGCGGCTCTCATCAACACCAACCTT 480
 AGGCGGGATGCCCTGCGCCACTGTCTTGACACCTCAAAGG 520
 CACGAGCTCTCATCTTTGGCAGTGAGATGGCCTCAGCTAT 560
 CTGTGAGATCCATGCTAGCCTGGAGCCCACACTCAGCCTC 600
 610 620 630 640
 TTCTGCTCTGGATCCTGGGAGCCCAGCACAGTGCCCGTCA 640
 GCACAGAGCATCTGGACCCTCTTCTGGAAGATGCCCCGAA 680
 GCACCTGCCCAGTCACCCAGACAAGGGTTTTACAGATAAG 720
 CTCTTCTACATCTACACATCGGGCACCACGGGGCTACCCA 760
 AAGCTGCCATTGTGGTGCACAGCAGGTATTATCGTATGGC 800
 810 820 830 840
 TTCCCTGGTGTACTATGGATTCCGCATGCGGCCTGATGAC 840
 ATTGTCTATGACTGCCTCCCCCTCTACCACTCAAGCAGGA 880
 AACATCGTGGGGATTGGCAGTGCTTACTCCACGGCATGAC 920
 TGTGGTGTATCCGGAAGAAGTTCTCAGCCTCCCGGTTCTGG 960
 GATGATTGTATCAAGTACAACCTGCACAGTGGTACAGTACA 1000
 1010 1020 1030 1040
 TTGGCGAGCTCTGCCGCTACCTCCTGAACCAGCCACCCCG 1040
 TGAGGCTGAGTCTCGGCACAAGGTGCGCATGGCACTGGGC 1080
 AACGGTCTCCGGCAGTCCATCTGGACCGACTTCTCCAGCC 1120
 GTTTCACATCCCCCAGGTGGCTGAGTTCTATGGGGCCAC 1160
 TGAATGCAACTGTAGCCTGGGCAACTTTGACAGCCGGGTG 1200

Fig. 68A

66E260"40550460

mmFATP4 full length.DNA

```

      1210      1220      1230      1240
      | | | | | | | | | | | | | | | |
GGGGCCTGTGGCTTCAATAGCCGCATCCTGTCCTTTGTGT 1240
ACCCTATCCGTTTGGTACGTGTCAATGAGGATACCATGGA 1280
ACTGATCCGGGGACCCGATGGAGTCTGCATTCCCTGTCAA 1320
CCAGGTCAGCCAGGCCAGCTGGTGGGTCGCATCATCCAGC 1360
AGGACCCTCTGCGCCGTTTCGACGGGTACCTCAACCAGGG 1400

      1410      1420      1430      1440
      | | | | | | | | | | | | | | | |
TGCCAACAACAAGAAGATTGCTAATGATGTCTTCAAGAAG 1440
GGGGACCAAGCCTACCTCACTGGTGACGTCCTGGTGATGG 1480
ATGAGCTGGGTTACCTGTACTTCCGAGATCGCACTGGGGA 1520
CACGTTCCGCTGGAAAGGGGAGAATGTATCTACCACTGAG 1560
GTGGAGGGCACACTCAGCCGCTGCTTCATATGGCAGATG 1600

      1610      1620      1630      1640
      | | | | | | | | | | | | | | | |
TGGCAGTTTATGGTGTGAGGTGCCAGGAAGTGAAGGCCG 1640
AGCAGGAATGGCTGCCGTTGCAAGTCCCATCAGCAACTGT 1680
GACCTGGAGAGCTTTGCACAGACCTTGAAAAAGGAGCTGC 1720
CTCTGTATGCCCCGCCCATCTTCTGCGCTTCTTGCCCTGA 1760
GCTGCACAAGACAGGGACCTTCAAGTTCAGAAAGACAGAG 1800

      1810      1820      1830      1840
      | | | | | | | | | | | | | | | |
TTGCGGAAGGAGGGCTTTGACCCATCTGTTGTGAAAGACC 1840
CGCTGTTCTATCTGGATGCTCGGAAGGGCTGCTACGTTGC 1880
ACTGGACCAGGAGGCCTATACCCGCATCCAGGCAGGCGAG 1920
GAGAAGCTGTGATTTCCCCCTACATCCCTCTGAGGGCCAG 1960
AAGATGCTGGATTTCAGAGCCCTAGCGTCCACCCCAAGGG 2000

      2010      2020      2030      2040
      | | | | | | | | | | | | | | | |
TCCTGGGCAATGCCAGACCAAAGCTAGCAGGGCCCCGCACC 2040
TCCGCCCCCTAGGTGCTGATCTCCCCCTCTCCCAAAGTCCA 2080
AGTGACTCACTGCCGCTTCCCCGACCCTCCAGAGGCTTTC 2120
TGTGAAAGTCTCATCCAAGCTGTGTCTTCTGGTCCAGGCG 2160
TGGCCCCCTGGCCCCAGGGTTTCTGATAGGCTCCTTTAGGA 2200

      2210      2220      2230      2240
      | | | | | | | | | | | | | | | |
TGGTATCTTGGGTCCAGCGGGCCAGGGTGTGGGAGAGGAG 2240
TCACTAAGATCCCTCCAATCAGAAGGGAGCTTACAAAGGA 2280
ACCAAGGCAAAGCCTGTAGACTCAGGAAGCTAAGTGGCCA 2320
GAGACTATAGTGGCCAGTCATCCCATGTCCACAGAGGATC 2360
TTGGTCCAGAGCTGCCAAAGTGTCACCTCTCCCTGCCTGC 2400

      2410      2420      2430      2440
      | | | | | | | | | | | | | | | |
ACCTCTGGGGAAAAGAGGACAGCATGTGGCCACTGGGCAC 2440
CTGTCTCAAGAAGTCAGGATCACACACTCAGTCCTTGTTT 2480
CTCCAGGTTCCCTTGTTCTTGTCTCGGGGAGGGAGGGACG 2520
AGTGTCTGTCTGTCTTCTGCCTGTCTGTGAGTCTGTG 2560
TTGCTTCTCCATCTGTCTTAGCCTGAGTGTGGGTGGAACA 2600

```

Fig. 68B

66E260" 10550460

mmFATP4 full length.DNA

2610 2620 2630 2640
GGCATGAGGAGAGTGTGGCTCAGGGGCCAATAAACTCTGC 2640
CTTGACTCCTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2680
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2710

Fig. 68C

09405504-092399

mmFATP4 full length.protein

10 20 30 40
MLLGASLVGALLFSKLVKLKPWTQVGFSLLLLYLGSGGWR 40
FIRVFIKTVRRDIFGGMVLLKVKTKVRRYLQERKTVPLLF 80
ASMVQRHPDKTALIFEGTDHWTFRQLDEYSSSVANFLQA 120
RGLASGNVVALFMENRNEFVGLWLGMAKLGVEAALINTNL 160
RRDALRHCLDTSKARALIFGSEMASAICEIHASLEPTLSL 200
210 220 230 240
FCSGSWEPSTVPVSTEHLDPILLEDAPKHLPSHPDKGFTDK 240
LFYIYTS GTTGLPKAAIVVHSRYRMASLVYYGFRMRPDD 280
IVYDCLPLYHSSRKHRGDWQCLLHGMTVVIRKKFSASRFW 320
DDCIKYNCTVVQYIGELCRYLLNQPPREAESRHKVVMALG 360
NGLRQSIWTD FSSRFHIPQVAEFYGATECNC SLGNFDSRV 400
410 420 430 440
GACGFNSRILSFVYPIRLVRVNEDTMELIRGPDGVCIPCQ 440
PGQPGQLVGRIIQQDPLRRFDGYLNQGANNKKIANDVFVK 480
GDQAYLTGDVLVMDLGYLYFRDRTGDTFRWKGENVSTTE 520
VEGTL S RLLHMADVAVYGVEVPGTEGRAGMAAVASPI S NC 560
DLESFAQTLKKELPLYARPIFLRFLPELHKTGTFFKFQKTE 600
610 620 630 640
LRKEGFDPSVVKDPLFYLDARKGCYVALDQEAYTRIQAGE 640
EKL. 644

Fig. 69

09405504.09350460

mmFATP5 full length.DNA

1 10 20 30 40
 CACTCATCAGAGCTAAGAGAGACTACACGCTCTCATCTAC 40
 TTCAGAAAGAGCCAATGCCATGGGTATTTGGAAGAACTA 80
 ACCTTACTGCTGTTGCTGCTTCTGCTGGTTGGCCTGGGGC 120
 AGCCCCCATGGCCAGCAGCTATGGCTCTGGCCCTGCGTTG 160
 GTTCCTGGGAGACCCACATGCCTTGTGCTGCTTGGCTTG 200
 210 220 230 240
 GCATTGCTGGGCAGACCCTGGATCAGCTCCTGGATGCCCC 240
 ACTGGCTGAGCCTGGTAGGAGCAGCTCTTACCTTATTCTT 280
 ATTGCCTCTACAGCCACCCCGAGGGCTACGCTGGCTGCAT 320
 AAAGATGTGGCTTTACCTTCAAGATGCTTTTCTATGGCC 360
 TAAAGTTCAGGCGACGCCTTAACAAACATCCTCCAGAGAC 400
 410 420 430 440
 CTTTGTGGATGCTTTAGAGCGGCAAGCACTGGCATGGCCT 440
 GACCGGGTGGCCTTGGTGTGTACTGGGTCTGAGGGCTCCT 480
 CAATCACAAATAGCCAGCTGGATGCCAGGTCTGTGAGGC 520
 AGCATGGGTCTGAAAGCAAAGCTGAAGGATGCCGTAATC 560
 CAGAACACAAGAGATGCTGCTATCTTAGTTCTCCCGT 600
 610 620 630 640
 CCAAGACCATTTCTGCTTTGAGTGTGTTTCTGGGGTTGGC 640
 CAAGTTGGGCTGCCCTGTGGCCTGGATCAATCCACACAGC 680
 CGAGGGATGCCCTTGCTACACTCTGTACGGAGCTCTGGGG 720
 CCAGTGTGCTGATTGTGGATCCAGACCTCCAGGAGAACCT 760
 GGAAGAAGTCCTTCCCAAGCTGCTAGCTGAGAACATTAC 800
 810 820 830 840
 TGCTTCTACCTTGGCCACAGCTCACCCACCCCGGGAGTAG 840
 AGGCTCTGGGAGCTTCCCTGGATGCTGCACCTTCTGACCC 880
 AGTACCTGCCAGCCTTCGAGCTACGATTAAGTGGAAATCT 920
 CCTGCCATATTATCTTTACTTCAGGGACCACTGGACTCC 960
 CAAAGCCAGCCATCTTATCACATGAGCGGGTCATACAAGT 1000
 1010 1020 1030 1040
 GAGCAACGTGCTGTCCTTCTGTGGATGCAGAGCTGATGAT 1040
 GTGGTCTATGACGTCCTACCTCTGTACCATACGATAGGGC 1080
 TTGTCTTGGATTCTTGGCTGCTTACAAGTTGGAGCCAC 1120
 CTGTGTCCTGGCCCCCAAGTTCTCTGCCTCCCGATTCTGG 1160
 GCTGAGTGCCGGCAGCATGGCGTAACAGTGATCTTGTATG 1200

Fig. 70A

65260"40550460

mmFATP5 full length.DNA

```

      1210      1220      1230      1240
      | | | | | | | | | | | | | | | |
TGGGTGAAATCCTGCGGTACTTGTGTAACGTCCCTGAGCA 1240
ACCAGAAGACAAGATACATACAGTGCGCTTGGCCATGGGA 1280
ACTGGACTTCGGGCAAATGTGTGGAACAACTTCCAGCAAC 1320
GCTTTGGTCCCATTCGGATCTGGGAATTCTACGGATCCAC 1360
AGAGGGCAATGTGGGCTTAATGAACTATGTGGGCCACTGC 1400

      1410      1420      1430      1440
      | | | | | | | | | | | | | | | |
GGGGCTGTGGGAAGGACCAGCTGCATCCTTCCAATGCTGA 1440
CTCCCTTTGAGCTTGTACAGTTCGACATAGAGACAGCAGA 1480
GCCTCTGAGGGACAAACAGGGTTTTTGCATTCTGTGGAG 1520
CCAGGAAAGCCAGGACTTCTTTTGACCAAGGTTGAAAGA 1560
ACCAACCCTTCTGGGCTACCGTGGTTCCCAGGCCGAGTC 1600

      1610      1620      1630      1640
      | | | | | | | | | | | | | | | |
CAATCGGAAACTTGTGCGAATGTACGACGCGTAGGAGAC 1640
CTGTACTTCAACACTGGGGACGTGCTGACCTTGGACCAGG 1680
AAGGCTTCTTCTACTTTCAAGACCGCCTTGGTGACACCTT 1720
CCGGTGGAAAGGGCGAAAACGTATCTACTGGAGAGGTGGAG 1760
TGTGTTTTGTCTAGCCTAGACTTCCTAGAGGAAGTCAATG 1800

      1810      1820      1830      1840
      | | | | | | | | | | | | | | | |
TCTATGGTGTGCCTGTGCCAGGGTGTGAGGGTAAGGTTGG 1840
CATGGCTGCTGTGAAACTGGCTCCTGGGAAGACTTTTGAT 1880
GGGCAGAAGCTATACCAGCATGTCCGCTCCTGGCTCCCTG 1920
CCTATGCCACACCTCATTTTCATCCGTATCCAGGATTCCT 1960
GGAGATCACAACACCTACAAGCTGGTAAAGTCACGGCTG 2000

      2010      2020      2030      2040
      | | | | | | | | | | | | | | | |
GTGCGTGAGGGTTTTGATGTGGGGATCATTGCTGACCCCC 2040
TCTACATACTGGACAACAAGGCCAGACCTTCCGGAGTCT 2080
GATGCCAGATGTGTACCAGGCTGTGTGTGAAGGAACCTGG 2120
AATCTCTGACCACCTAGCCAAGTGAAGGCAATCCAAAAG 2160
TGTAGAGATTGACACTAGTCAGCTTCACAAAGTTGTCCGG 2200

      2210      2220      2230      2240
      | | | | | | | | | | | | | | | |
GTTCCAGATGCCCATGGCCCAGTAGTACTTAGAGAATAAA 2240
CTTGAATGTGTATACAAAAA 2277

```

Fig. 70B

66E260" 40550460

mmFATP5 full length.protein

10 20 30 40
 MGIWKKLTLLLLLLLLVGLGQPPWPAAMALALRWFLGDP 40
 CLVLLGLALLGRPWISSWMPHWLSLVGAALTFLLLPLQPP 80
 PGLRWLHKDVAFTFKMLFYGLKFRRRLNKHPPETFVDALE 120
 RQALAWPDRVALVCTGSEGSSITNSQLDARSCQAAWVLKA 160
 KLKDAVIONTRDAAAAILVLPSTISALSVFLGLAKLGCPV 200
 210 220 230 240
 AWINPHSRGMPLLLHSVRSSGASVLIVDPDLQENLEEVLPK 240
 LLAENIHCFYLGHSSTPGVEALGASLDAAPSDPVPASLR 280
 ATIKWKSPAIFIFTSGTTGLPKPAILSHERVIOVSNVLSF 320
 CGCRADDVVYDVLPLYHTIGLVGLGCLQVGATCVLAPK 360
 FSASRFWAECRQHGVTVILYVGEILRYLCNVPEQPEDKIH 400
 410 420 430 440
 TVRLAMGTGLRANVWKNFQQRFGPIRIWEFYGSTEGNVGL 440
 MNYVGHCGAVGRTSCILRMLTPFELVQFDIETAELRDKQ 480
 GFCIPVEPGKPGLLLTKVRKNQPFLLGYRGSQAESNRKLVA 520
 NVRRVGDLYFNTGDVLTLDQEGFFYFQDRLGDTFRWKGEN 560
 VSTGEVECVLSSLDLEEVDVYGVVPGCEGKVGMAAVKL 600
 610 620 630 640
 APGKTFDGQKLYQHVRSWLPAYATPHFIRIQDSLEITNTY 640
 KLVKSRLVREGFDVGIIADPLYILDNKAQTFRSLMPDVYQ 680
 AVCEGTWNL. 690

Fig. 71

00550409260

dmFATP partial.DNA

1 10 20 30 40
GCTCTCTGGGCTATATCAAGCTGCTGAGGTACACGAAGC 40
GCCATGAGCGGCTCAACTACACGGTGGCGGACGTCTTCGA 80
ACGAAATGTTTCAGGCCCATCCGGACAAGGTGGCTGTGGTC 120
AGTGAGACGCAACGCTGGACCTTCCGTCAGGTGAACGAGC 160
ATGCGAACAAGGTGGCCAATGTGCTGCAGGCTCAGGGCTA 200

210 220 230 240
CAAAAAGGGCGATGTGGTGGCCCTGTTGCTGGAGAACCGC 240
GCCGAGTACGTGGCCACCTGGCTGGGTCTCTCCAAGATCG 280
GTGTGATCACACCGCTGATCAACACGAATCTGCGCGGTCC 320
CTCCCTGCTGCACAGCATCACGGTGGCCCATTTGCTCGGCT 360
CTCATTTACGGCGAGGACTTCCTGGAAGCTGTCACCGACG 400

410 420 430 440
TGGCCAAGGATCTGCCAGCGAACCTCACACTCTTCCAGTT 440
CAACAACGAGAACAACAACAGCGAGACGGAAAAGAACATA 480
CCGCAGGCCAAGAATCTGAACGCGCTGCTGACCACGGCCA 520
GCTATGAGAAGCCTAACAAGACGCAGGTTAACCACCACGA 560
CAAGCTGGTCTACATCTACACCTCCGGCACCACAGGATTG 600

610 620 630 640
CCAAAGGCTGCGGTTATCTCTCACTCCCGTTATCTGTTTA 640
TCGCTGCTGGCATCCACTACACCATGGGTTTCCAGGAGGA 680
GGACATCTTCTACACGCCCTTGCCCTTTGTACCACACCGCT 720
GGTGGCATTATGTGCATGGGTGAGTCGGTGCTCTTTGGCT 760
CCACGGTCTCCATTTCGCAAGAAGTTCTCGGCATCCAATA 800

810 820 830 840
TTTCGCCGACTGCGCCAAGTATAATGCAACTATTGGTCAG 840
TATATCGGTGAGATGGCTCGCTACATTCTAGCTACGAAAC 880
CCTCGGAATACGACCAGAAACACCGAGTGCGTCTGGTCTT 920
TGGAACGGACTGCGACCGCAGATTTGGCCACAGTTTGTG 960
CAGCGCTTCAACATTGCCAAGGTTGGCGAGTTCTACGGCG 1000

1010 1020 1030 1040
CCACCGAGGGTAATGCGAACATCATGAATCATGACAACAC 1040
GGTGGGCGCCATCGGCTTTGTGTCGCGCATCCTGCCCAAG 1080
ATCTACCGAATCTCGATCATTTCGCGCCGATCCGGACACCG 1120
GAGAGCCCATTAGAGATAGGAATGGCCTATGCCAACTGTG 1160
CGCTCCCAACGAGCCAGGCGTATTTCATCGGCAAGATCGTC 1200

Fig. 72A

09405504.09399

dmFATP partial.DNA

1210 1220 1230 1240
 AAAGGAAATCCTTCTCGCGAATTCCTCGGATACGTCGATG 1240
 AAAAGGCCTCCGCGAAGAAGATTGTTAAGGATGTGTTCAA 1280
 GCATGGCGATATGGCTTTTCATCTCCGGAGATCTGCTGGTT 1320
 GCGGACGAGAAGGGTTATCTGTACTTCAAGGATCGCACCG 1360
 GTGACACCTTCCGCTGGAAGGGCGAGAATGTTTCCACCAG 1400

1410 1420 1430 1440
 CGAGGTGGAGGCGCAAGTCAGCAATGTGGCCGGTTACAAG 1440
 GATACCGTCGTTTACGGCGTAACCATTCGCGACACCGAGG 1480
 GAAGGGCCGGCATGGCCGCCATCTATGATCCGGAGCGAGA 1520
 ATTGGACCTCGACGTCTTCGCCGCTAGCTTGGCCAAGGTG 1560
 CTGCCCCGCTACGCTCGTCCCCAGATCATTGATTGCTCA 1600

1610 1620 1630 1640
 CCAAGGTGGACCTGACTGGAACCTTTAAGCTGCGCAAGGT 1640
 AGACCTGCAGAAGGAGGGCTACGATCCGAACGCGATCAAG 1680
 GACGCGCTGTACTACCAGACTTCCAAGGGTCGGTACGAGC 1720
 TGCTCAGCCCCAGGTTTACGACCAGGTGCAGCGCAACGA 1760
 AATCCGCTTCTAAGAGCTGCAATAGAGTTGTGTCTGAACC 1800

1810 1820 1830 1840
 TTGCCTTTTGCCCAATATGCTGTTAATTAGTTTGTAAAGGC 1840
 TAAGTGTAGTAGAGGAAAAATCGGGGAAATCGGCAGCAAA 1880
 GATCATTACGCCTAGGAGAGATGCATCCGAAGCACATTTTC 1920
 CATGTCAACAATGCACTTTTGTATATCGTAAGCATATATA 1960
 TATCGTATATCGTAAACGTAGTTGTATCTGCATTTGTGTA 2000

2010 2020 2030 2040
 GATGATAGCCTCCTATACGCATTTCAATTGTTTTTAGCGT 2040
 GCTAAAGAACCTTGTTAAATGCAATTTTCAGCTATTGTTTA 2080
 GTCAGTTTTAGTGGCATTACACTTCCATTCTCGTTGCGT 2120
 TTCGTTTTTGCTGTACATATGAGAAGCTCTGATGTTTTT 2160
 GTATCAAATAAAGTTTTTTCCTTACCACGGACCACGTGA 2200

2210 2220 2230 2240
 AAAAAAAAAAAAAAAAAAAAAA 2221

Fig. 72B

09405504 "40550460

dmFATP partial.protein

10 20 30 40
 ALWAYIKLLRYTKRHERLNYTVADVFERNVQAHPDKVAVV 40
 SETQRWTFRQVNEHANKVANVLQAQGYKKGDVALLLENR 80
 AEYVATWLGLSKIGVITPLINTNLRGPSLLHSITVAHCSA 120
 LIYGEDFLEAVTDVAKDLPANLTLFQFNENNNNSETEKNI 160
 POAKNLNALLTTASYEKPNTQVNHHDKLVIYITSGTTGL 200
 210 220 230 240
 PKAAVISHSRYLFIAAGIHYTMGFQEEDIFYTPLPLYHTA 240
 GGIMCMGQSVLFGSTVSIRKKFSASNYFADCAKYNATIGQ 280
 YIGEMARYILATKPSEYDQKHRVRLVFGNGLRPQIWPQFV 320
 QRFNIAKVGEFYGATEGNANIMNHDNTVGAIGFVSRILPK 360
 IYPISIIRADPDTGEPIDRNLGLCQLCAPNEPGVFIGKIV 400
 410 420 430 440
 KGNPSREFLGYVDEKASAKKIVKDVFKHGDMAFISGDLLV 440
 ADEKGYLYFKDRTGDTFRWKGENVSTSEVEAQVSNVAGYK 480
 DTVVYGV TIPHTEGRAGMAAIYDPERELDLVFAASLAKV 520
 LPAYARPQIIIRLLTKVDLTGTFKLRKVDLQKEGYDPNAIK 560
 DALYYQTSKGRYELLTPQVYDQVQRNEIRF 590

Fig. 73

09405504.092399

drFATP partial.DNA

1 10 20 30 40

AGTGTAGATACACAGGAACGTTTAAAATCCAGAAGACCA 40
GACTGCAAAGGGAAGGATACGATCCACGGCTCACAACCTGA 80
CCAGATCTACTTCCTAAACTCCAGAGCAGGGCGTTACGAG 120
CTTGTCAACGAGGAGCTGTACAATGCATTTGAACAAGGGC 160
AGGATTTCCCTTT 173

Fig. 74

09405504.092399

drFATP partial.protein

10 20 30 40
SVDTTGTFKIQKTRLQREGYDPRLTTDQIYFLNSRAGRYE 40
LVNEELYNAFEQGQDFP 57

Fig. 75

0044554.092390
66260"10554460

ceFATPa coding only.DNA

1 10 20 30 40
 ATGAAGCTGGAGGAGCTTGTGACAGTTATGCTTCTCACAG 40
 TGGCTGTCAATTGCTCAGAATCTTCCGATTGGAGTAATATT 80
 GGCTGGAGTTCTTATTTTATACATCACAGTGGTTCATGGA 120
 GATTTTCATTTATAGAAGTTATCTTACGTTGAATAGGGATT 160
 TAACAGGATTGGCTCTAATTATTGAAGTCAAAATCGACCT 200
 210 220 230 240
 ATGGTGGAGGTTGCATCAGAATAAAGGAATCCATGAAGT 240
 TTTTGGATATTGTGAAAAAGAATCCAAATAAGCCGGCGA 280
 TGATTGACATCGAGACGAATACAACAGAAACATACGCAGA 320
 GTTCAATGCACATTGTAATAGATATGCCAATTATTTCCAG 360
 GGTCTTGGCTATCGATCCGGAGACGTTGTCGCCTTGTACA 400
 410 420 430 440
 TGGAGAACTCGGTTCGAGTTTGTGGCCGCGTGGATGGGACT 440
 CGCAAAAATCGGAGTTGTAACGGCTTGGATCAACTCGAAT 480
 TTGAAAAGAGAGCAACTTGTTCATTGTATCACTGCGAGCA 520
 AGACAAAGGCGATTATCACAAGTGTAACACTTCAGAATAT 560
 TATGCTTGATGCTATCGATCAGAAGCTGTTTGATGTTGAG 600
 610 620 630 640
 GGAATTGAGGTTTACTCTGTCTGGAGAGCCCAAGAAGAATT 640
 CTGGATTCAAGAATCTCAAGAAGAAGTTGGATGCTCAAAT 680
 TACTACGGAACCAAGACCCTTGACATAGTAGATTTTAAA 720
 AGTATTCTTTGCTTCATCTATACAAGTGGTACTACTGGAA 760
 TGCCAAAAGCCGCTGTCTATGAAGCACTTCAGATATTACTC 800
 810 820 830 840
 GATTGCCGTTGGAGCCGCAAAATCATTCCGAATCCGCCCT 840
 TCTGATCGTATGTACGTCGATGCCAATTTATCACACTG 880
 CAGCTGGAATTCTTGGAGTTGGGCAAGCTCTGTTGGGTGG 920
 ATCATCGTGTGTCATTAGAAAAAATTCTCGGCTAGCAAC 960
 TTTTGGAGGGATTGTGTAAAGTATGATTGTACAGTTTCAC 1000
 1010 1020 1030 1040
 AATACATTGGAGAGATTTGTCTGGTACTTGTGGCTCAGCC 1040
 AGTTGTGGAAGAGGAATCCAGGCATAGAATGAGATTGTTG 1080
 GTTGGAAACGGACTCCGTGCTGAAATCTGGCAACCATTTG 1120
 TAGATCGATTCCGTGTCAGAATTGGAGAACTTTATGGTTC 1160
 AACTGAAGGAACTTCATCTCTCGTGAACATTGACGGACAT 1200

Fig. 7cA

66E260-40550-460

09-10504-09

Fig. 76B

ceFATPa coding only.protein

...

10	20	30	40
MKEELVTVMLLTVAIVIAQNLPIGVILAGVLILYITVVHG 40			
DFIYRSYLTNRLDTGLALITIEVKIDLWRLHONKGIHEL 80			
FLDIVKKPNKPNKAMIDIETNTTETYAEFNAHCNRYANYFQ 120			
GLGYRSGDVVALYMENSVEFVAAWMGLAKIGVVTAWINSN 160			
LKREQLVHCITASKTKAIIITSVTLQNIMLDAIDQKLFDE 200			
210	220	230	240
GIEVYSVGEPKKNSGFKNLKKKLDAQITTEPKTLDIVDFK 240			
SILCFIYTS GTTGMPKAAVMKHFRYYSAVGAAKSFGIRP 280			
SDRMYSMPPIYHTAAGILGVGOALLGGSSCVIRKKFSASN 320			
FWRDCVKYDCTVSQYIGEICRYLLAQPVEEESRHRMRL 360			
VGNGLRAEIQPFVDRFRVRIGELYGSTEGTSSLVNIDGH 400			
410	420	430	440
VGACGFLPISPLTKKMHPVRLIKVDDVTGEAIRTSDGLCI 440			
ACNPGESGAMVSTIRKNNPLLQFEGYLNKKETNKKIIRDV 480			
FAKGDSCFLTGDLLHWDRLLGYVYFKDRTGDTFRWKGENVS 520			
TTEVEAILHPITGLSDATVYGVEVPQREGRVGMASVVRVV 560			
SHEEDETQFVHRVGARLASSLTSYAIPQFMRICQDVEKTG 600			
610	620	630	640
TFKLVKTNLQRLGIMDAPSDSIYIYNSENRNFPFNDLR 640			
CKVSLGSYPF. 651			

Fig. 77

0940504-0939

10 20 30 40
 ATGAGGGAAATGCCGGACAGTCCCAAGTTTGC GTTAGTCA 40
 CGTTTGTGTGTATGCAGTGGTTTTGTACAATGTCAACAG 80
 CGTTTTCTGGAAATTTGTATTCATCGGATATGTTGTATTT 120
 AGGCTGCTTCGCACTGATTTTGGAGAAGAGCACTTGCCA 160
 CGTTACCTAGAGATTTTGC GGGACTGAAGCTCTTAATATC 200
 210 220 230 240
 GGTAAAGTCGACAATTCGTGGCTTGTTCAAGAAAGATCGC 240
 CCAATTCATGAAATCTTTTTGAATCAGGTGAAACAGCATC 280
 CAAACAAAGTGGCGATTATTGAAATTGAAAGTGGTAGGCA 320
 GTTGACGTATCAAGAATTGAATGCGTTAGCTAATCAGTAT 360
 GCTAACCTTTACGTGAGTGAAGGTTACAAAATGGGCGACG 400
 410 420 430 440
 TTGTCGCTTTGTTTATGGAAAATAGCATCGACTTCTTTGC 440
 AATTTGGCTGGGACTTTCCAAGATTGGAGTCGTGTCGGCG 480
 TTCATCAACTCAAACCTTGAAGTTGGAGCCATTGGCACATT 520
 CGATTAATGTTTCGAAGTGCAAATCATGCATTACCAATAT 560
 CAATCTGTTGCCGATGTTCAAAGCCGCTCGTGAAAAGAAT 600
 610 620 630 640
 CTGATCAGTGACGAGATCCACGTGTTTCTGGCTGGAAGTC 640
 AGGTTGATGGACGTCATAGAAGTCTTCAGCAAGATCTCCA 680
 TCTTTTCTCTGAGGATGAACCTCCAGTTATAGACGGACTC 720
 AATTTTAGAAGCGTTCTGTGTTATATTTACACTTCCGGTA 760
 CTACCGGAAATCCAAAGCCAGCCGTCATTAAACACTTCCG 800
 810 820 830 840
 TTACTTCTGGATTGCGATGGGAGCAGGAAAAGCATTGGA 840
 ATTAATAAGTCAGACGTTGTGTACATTACGATGCCAATGT 880
 ATCACTCTGCCGCCGGTATCATGGGTATTGGATCATTAAT 920
 TGCATTGGGTCGACCGCTGTTATTAGGAAAAAGTTTTTCG 960
 GCAAGCAACTTCTGGAAAGATTGCGTCAAGTACAACGTCA 1000
 1010 1020 1030 1040
 CAGCGACACAGTACATTGGAGAAATCTGCAGGTATCTTCT 1040
 GGCAGCGAATCCATGTCCTGAAGAGAAACAACACAACGTG 1080
 CGATTGATGTGGGGAAATGGTTTGAGAGGACAAATTTGGA 1120
 AAGAGTTTGTAGGAAGATTTGGAATTAAGAAAATTGGAGA 1160
 GTTGTACGGCTCAACAGAAGGAAACTCCAATATTGTTAAC 1200

Fig. 78A

0 9 4 0 8 3 1 0 2 9 9

Fig. 78B

ceFATPb coding only.protein

10 20 30 40
MREMPDSPKFALVTFVVYAVVLYNVNSVFWKFVFIGYVVF 40
RLLRTDFGRRALATLPRDFAGLKLLISVKSTIRGLFKKDR 80
PIHEIFLNQVKQHPNKVAIEIESGRQLTYQELNALANQY 120
ANLYVSEGYKMGDVVALFMENSIDFFAIWLGLSKIGVISA 160
FINSNLKLEPLAHSINVSCKSCITNINLLPMFKAAREKN 200
210 220 230 240
LISDEIHVFLAGTQVDGRHRSLLQDLHLFSEDEPPVIDGL 240
NFRSVLCYIYTSGTTGNPKPAVIKHFYFWIAMGAGKAFG 280
INKSDVVYITMPMYHSAAGIMGIGSLIAFGSTAVIRKKFS 320
ASNFWKDCVKYNVTATQYIGEICRYLLAANPCPEEKQHN 360
RLMWGNGLRGQIWKEFVGRFGIKKIGELYGSTEGNSNIVN 400
410 420 430 440
VDNHVGACGFMPYIPHIGSLYPVRLIKVD RATGELERDKN 440
GLCVPCVPGETGEMVGVIKEKDILLKFEGYVSEGDTAKKI 480
YRDVFKHGDKVFASGDILHWDDLGYLYFVDRCGDTFRWKG 520
ENVSTTEVEGILQPVMDVEDATVYGVTVGKMEGRAGMAGI 560
VVKDGTDOVEKFIADITSRLTENLASAIPVFI RLCKEVDR 600
610 620 630 640
TGTFKLKKTDLQKQGYDLVACKGDPIYYWSAAEKSYPKPLT 640
DKMQQDIDTGVYDRI. 656

Fig. 79

66E260"40550460

10 20 30 40
 ATGGCGTGTATGCATCAGGCTCAGCTATACAATGATCTAG 40
 AGGAATTGCTAACTGGTCCATCAGTACCCATCGTTGCTGG 80
 AGCTGCTGGAGCTGCAGCTCTCACTGCCTACATTAACGCC 120
 AAATACCACATAGCCCATGATCTCAAGACCCTCGGTGGTG 160
 GATTGACACAATCGTCCGAAGCGATTGATTTTCATAAACCG 200

210 220 230 240
 CCGCGTGCACAAAAGCGCGTCTCAGCACCACATCTTC 240
 CAGGAGCAGGTCCAAAAACAATCAAATCATCCCTTTCTTA 280
 TCTTTGAGGGCAAGACATGGTCTTACAAGGAGTTCTCTGA 320
 GGCATACACGAGGGTGCAGAACTGGCTGATTGATGAGCTG 360
 GACGTACAAGTAGGGGAGATGGTCGCAATTGATGGCGGAA 400

410 420 430 440
 ATAGTGCAGAGCACCTGATGCTTTGGCTTGCACTTGATGC 440
 AATCGGTGCGGTACGAGTTTTTTGAACTGGAACCTGACA 480
 GGGGCAGGGTTAATTCATTGCATAAAGCTATGCGAATGTC 520
 GATTCTTATCGCAGACATCGATATTAAGCGAACATTGA 560
 ACCGTGCCGTGGCGAACTGGAGGAGACGGGCATCAACATT 600

610 620 630 640
 CACTACTATGACCCATCCTTCATCTCATCGCTACCGAATA 640
 ACACGCCAATTCCCGACAGCCGCACTGAGAACATTGAATT 680
 AGATTCACTACGAGGACTGATATACACATCTGGAACCACT 720
 GGTCTACCTAAAGGCGTGTTTATAAGCACTGGCCGCGAGC 760
 TTAGGACTGACTGGTTCGATTTCAAAGTATCTAAATCTCAA 800

810 820 830 840
 GCCCACGGATCGAATGTATACATGTATGCCGCTCTACCAT 840
 GCCGCTGCACACAGCCTCTGTACAGCATCAGTTATTCATG 880
 GTGGAGGTACCGTGGTATTGAGCAGGAAATTCTCACACAA 920
 GAAGTTCTGGCCTGAAGTTGTGGCTTCGGAAGCAAATATC 960
 ATTCAGTACGTTGGTGAATTAGGTCGATATCTCCTGAATG 1000

1010 1020 1030 1040
 GTCCAAAGAGTCCTTACGACAGGGCCCATAAAGTCCAGAT 1040
 GCGGTGGGGCAATGGCATGCGTCCAGACGTGTGGGAAGCG 1080
 TTTCGTGAACGCTTCAACATACCAATTATTTCATGAGCTCT 1120
 ATGCCGCAACCGATGGGCTCGGGTCAATGACCAATCGTAA 1160
 CGCGGGCCCTTTTACAGCAAACCTGATTGCGCTGCGAGGG 1200

Fig. 80A

09405504 092399

[illegible]

Fig. 80B

chFATP coding only.protein

1

10 20 30 40

MACMHQAQLYNDLEELLTGPSVPIVAGAAGAAALTAYINA 40
KYHIAHDLKTLGGGLTQSSEAIIDFINRRVAQKRVLTHHIF 80
QEQVQKQSNHPFLIFEGKTWSYKEFSEAYTRVANWLIDEL 120
DVQVGEMVAIDGGNSAEHMLWLALDAIGAATSFLNWNLT 160
GAGLIHCIKLCECRFVIADIDIKANIEPCRGELEETGINI 200

210 220 230 240

HYDPSFISSLPNNTPIPDSRTENIELDSVRGLIYTS GTT 240
GLPKGVIISTGRELRTDWSISKYLNKPTDRMYTCMP LYH 280
AAAHSLCTASVIHGGGTVVLSRKFSHKKFWPEVVASEANI 320
IQYVGELGRYLLNGPKSPYDRAHKVQMAWGNGMRPDVWEA 360
FRERFNIPIIHELAAATDGLGSM TNRNAGPFTANCIALRG 400

410 420 430 440

LIWHWKFRNQEVLYKMDLDTDEIMRDRNGFAIRCAVNEPG 440
QMLFRLTPETLAGAPSYNNETATQSRRITDVFQKGDLWF 480
KSGDMLRQDAEGRVYFVDRLGDTFRWKSENVSTNEVADVM 520
GTFPQIAETNVYGVLPVGNDRVRS LNCHGRRRDRVDIRF 560
AALAKHARDRLPGYAVPLFLRVTPALEYTGTLKIQKGRLK 600

610 620 630 640

QEGIDPKISGEDKLYWLPPGSDIYLPFGKMEWQGIVDKR 640
IRL 643

Fig. 81

004055040550460

```

      10      20      30      40
      |      |      |      |
CTTTACCATTCATCAGCTTCATTCTGCATTTTGTAGCTTGA 40
CGGCAGCCGGGTCTACGCTGATCATCGGCCGCAAGTTCTC 80
CGCGAGAACTTCATAAAGGAAGCGCGCGAGAACGACGCC 120
ACGGTCATCCAGTACGTGGGTGAGACCTTGCGATATCTGC 160
TCGCCACCCCGGTGAAACCGATCCAGTTACTGGCGAAGA 200

      210      220      230      240
      |      |      |      |
CCTGGACAAAAAGCACAATATTTCGAGCAGTATACGGCAAC 240
GGGCTACGGCCGGATATCTGGAACCGCTTCAAGGAGCGCT 280
TCAACGTGCCGACGGTTGCCGAATTTTATGCTGCAACCGA 320
GAGCCCAGGCGGAACATGGAACATTTCAACAAATGACTTC 360
ACTGCCGGAGCCATTGGGCACACTGGCGTGCTTAGTGGAT 400

      410      420      430      440
      |      |      |      |
GGCTTCTTGGACGCGGCCTTACTATTGTGCGAGGTGGACCA 440
GGAATCACAGGAACCATGGCGCGATCCCCAAACCGGGTTC 480
TGCAAGCCGGTCCCGCGAGGCGAAGCAGGCGAGCTCCTGT 520
ATGCCATTGATCCGGCCGACCCGGGCGAGACCTTCCAGGG 560
CTACTACCGCAACTCCTTTAGAGCACACTGGCGGCCG 597

```

Fig. 82

aspergillus partial.protein

10 20 30 40
LYHSSASFCIFSLTAAGSTLIIGRKFSARNFIKEAREND 40
TVIQYVGETLRYLLATPGETDPVTGEDLDKKNIRAVYGN 80
GLRPDIWNRFKERFNVPTVAEFYAATESPGGTWNYSTNDF 120
TAGAIGHTGVLSGWLLGRGLTIVEVDQESQEPWRDPQTGF 160
CKPVPRGEAGELLYAIDPADPGETFQGYRNSFRAHWRP 199

Fig. 83

09405504.092399

Fig. 84

mgFATP partial.protein

10 20 30 40

AKADAWLRTGNVIRADNEGRLFFHDIRIGDTFRWKGETVST 40
QEVSLVLGRHDSIKEANVYGVTVPNHDGRAGCAALTLSDA 80
LATEKKLGDELLKGLATHSSTSLPKFAVPQFLRVVRGEMQ 120
STGTNKQQKHDLRVQGVPEPGKVGDEVYWLRRGGTYVPFGT 160
EDWDGLKKGLVKL 173

Fig. 85

66E26D "HDS50460

10 20 30 40
ATGTCTCCCATACAGGTTGTTGTCTTTGCCTTGTCAAGGA 40
TTTTCTGCTATTATTTCAGACTTATCAAGCTAATTATAAC 80
CCCTATCCAGAAATCACTGGGTTATCTATTTGGTAATTAT 120
TTTGATGAATTAGACCGTAAATATAGATACAAGGAGGATT 160
GGTATATTATTCCTTACTTTTTGAAAAGCGTGTTTTGTTA 200
210 220 230 240
TATCATTGATGTGAGAAGACATAGGTTTCAAACTGGTAC 240
TTATTTATTAAACAGGTCCAACAAAATGGTGACCATTTAG 280
CGATTAGTTACACCCGTCCCATGGCCGAAAAGGGAGAATT 320
TCAACTCGAAACCTTTACGTATATTGAACTTATAACATA 360
GTGTTGAGATTGTCTCATATTTTGCATTTTGATTATAACG 400
410 420 430 440
TTCAGGCCGGTGACTACGTGGCAATCGATTGTACTAATAA 440
ACCTCTTTTCGTATTTTTATGGCTTTCTTTGTGGAACATT 480
GGGGCTATTCCAGCTTTTTTAACTATAATACTAAAGGCA 520
CTCCGCTGGTTCACCTCCCTAAAGATTTCCAATATTACGCA 560
GGTATTTATTGACCCGTGATGCCAGTAATCCGATCAGAGAA 600
610 620 630 640
TCGGAAGAAGAAATCAAAAACGCACCTTCCTGATGTAAAT 640
TAACTATCTTGAAGAACAAGACTTAATGCATGAACTTTT 680
AAATTCGCAATCACCGGAATTCTTACAACAAGACAACGTT 720
AGGACACCACTAGGCTTGACCGATTTTAAACCCTCTATGT 760
TAATTTATACATCTGGAACCACTGGTTTGCCTAAATCCGC 800
810 820 830 840
TATTATGTCTTGGAGAAAATCCTCCGTAGGTTGTCAAGTT 840
TTTGGTCATGTTTTACATATGACTAATGAAAGCACTGTGT 880
TCACAGCCATGCCATTGTTCCATTCAACTGCTGCCTTATT 920
AGGTGCGTGCGCCATTCTATCTCACGGTGGTTGCCTTGCG 960
TTATCGCATAAATTTTCTGCCAGTACATTTTGAAGCAAG 1000
1010 1020 1030 1040
TTTATTTAACAGGAGCCACGCACATCCAATATGTCGGAGA 1040
AGTCTGTAGATACCTGTTACATACGCCAATTTCTAAGTAT 1080
GAAAAGATGCATAAGGTGAAGGTTGCTTATGGTAACGGGC 1120
TGAGACCTGACATCTGGCAGGACTTCAGGAAGAGGTTCAA 1160
CATAGAAGTTATTGGTGAATTCTATGCCGCAACTGAAGCT 1200

Fig. 86A

scFATP coding only.DNA

1210	1220	1230	1240
CCTTTTGCTACAACCTACCTTCCAGAAAGGTGACTTTGGAA 1240			
TTGGCGCATGTAGGAACCTATGGTACTATAATTCAATGGTT 1280			
TTTGTCATTCCAACAAACATTGGTAAGGATGGACCCAAAT 1320			
GACGATTCCGTTATATATAGAAATTCCAAGGGTTTCTGCG 1360			
AAGTGGCCCCCTGTTGGCGAACCAGGAGAAATGTTAATGAG 1400			
1410	1420	1430	1440
AATCTTTTTCCCTAAAAAACCAGAAACATCTTTTCAAGGT 1440			
TATCTTGGAATGCCAAGGAAACAAAGTCCAAAGTTGTGA 1480			
GGGATGTCTTCAGACGTGGCGATGCTTGGTATAGATGTGG 1520			
AGATTTATTTAAAGCGGACGAATATGGATTATGGTATTTT 1560			
CTTGATAGAATGGGTGATACTTTCAGATGGAAATCTGAAA 1600			
1610	1620	1630	1640
ATGTTTCCACTACTGAAGTAGAAGATCAGTTGACGGCCAG 1640			
TAACAAAGAACAATATGCACAAGTTCTAGTTGTTGGTATT 1680			
AAAGTACCTAAATATGAAGGTAGAGCTGGTTTTGCAGTTA 1720			
TTAAACTAACTGACAACTCTCTTGACATCACTGCAAAGAC 1760			
CAAATTATTAAATGATTTCCTTGAGCCGGTTAAATCTACCG 1800			
1810	1820	1830	1840
TCTTATGCTATGCCCCTATTTGTTAAATTTGTTGATGAAA 1840			
TTAAATGACAGATAACCTCATAAAATTTTGA 1872			

Fig. 86B

66260"40550460

scFATP coding only.protein

06E260"40550460

10 20 30 40
MSPIQVVVFALSRIFLLLFRLIKLIITPIQKSLGYLFGNY 40
FDELORKYRYKEDWYIIPYFLKSVFCYIIDVRRHRFQNWY 80
LFIKQVQONGDHLAISYTRPMAEKGEFQLETFTYIETYN 120
VLRLSHILHFDYNVQAGDYVAIDCTNKPLFVFLWLSLWNI 160
GAIPAFLNYNTKGTPLVHSLKISNITQVFIDPDASNPIRE 200
210 220 230 240
SEEEIKNALPDVKLNYLEEQDLMHELLNSQSPEFLQQDNV 240
RTPLGLTDFKPSMLIYTSGTTGLPKSAIMSWRKSSVGCQV 280
FGHVLHMTNESTVFTAMPLFHSTAALLGACAILSHGGCLA 320
LSHKFSASTFWKQVYLTGATHIQYVGEVCRYLLHTPIISKY 360
EKMHKVKVAYGNLRLPDIWQDFRKRFRNIEVIGEFYAATEA 400
410 420 430 440
PFATTTFQKGDFGIGACRNYGTIIQWFLSFQQTIVRMDPN 440
DDSVIYRNSKGFCEVAPVGEPEGEMLMRIFFPKKPETSFGQ 480
YLGNAKETKSKVVRDVFRRGDAWYRCGDLLKADEYGLWYF 520
LDRMGDTFRWKSENVSTTEVEDQLTASNKEQYAQVLVVG 560
KVPKYEGRAFAVIKLTDNSLDITAKTKLLNDSLRLNLP 600
610 620 630 640
SYAMPLFVKFVDEIKMTDNLIK. 624

Fig. 87

10 20 30 40
 GTGTCCGATTACTACGGCGGGCGCACACACAACGGTCAGGC 40
 TGATCGACCTGGCAACTCGGATGCCGCGAGTGTTGGCGGA 80
 CACGCCGGTGATTGTGCGTGGGGCAATGACCGGGCTGCTG 120
 GCGCGGCCGAATTCCAAGGCGTCGATCGGCACGGTGTTCC 160
 AGGACCGGGCCGCTCGCTACGGTGACCGAGTCTTCCTGAA 200
 210 220 230 240
 ATTCGGCGATCAGCAGCTGACCTACCGCGACGCTAACGCC 240
 ACCGCCAACCGGTACGCCGCGGTGTTGGCCGCCCGCGGCG 280
 TCGGCCCCGGCGACGTCGTTGGCATCATGTTGCGTAACTC 320
 ACCCAGCACAGTCTTGGCGATGCTGGCCACGGTCAAGTGC 360
 GGGCGTATCGCCGGCATGCTCAACTACCACCAGCGCGGCG 400
 410 420 430 440
 AGGTGTTGGCGCACAGCCTGGGTCTGCTGGACGCGAAGGT 440
 ACTGATCGCAGAGTCCGACTTGGTCAGCGCCGTCGCCGAA 480
 TGCGGCGCCTCGCGCGGCCGGGTAGCGGGCGACGTGCTGA 520
 CCGTCGAGGACGTGGAGCGATTGCCACAACGGCGCCCGC 560
 CACCAACCCGGCGTCGGCGTGGCGGTGCAAGCCAAAGAC 600
 610 620 630 640
 ACCGCGTTCTACATCTTCACCTCGGGCACCACCGGATTTT 640
 CCAAGGCCAGTGTCATGACGCATCATCGGTGGCTGCGGGC 680
 GCTGGCCGTCTTCGGAGGGATGGGGCTGCGGCTGAAGGGT 720
 TCCGACACGCTCTACAGCTGCCTGCCGCTGTACCACAACA 760
 ACGCGTTAACGGTCGCGGTGTCGTCGGTGATCAATTCTGG 800
 810 820 830 840
 GGCGACCCTGGCGCTGGGTAAGTCGTTTTCGGCGTCGCGG 840
 TTCTGGGATGAGGTGATTGCCAACCAGGGCGACGGCGTTTC 880
 TCTACATCGGCGAAATCTGCCGTTATCTGCTCAACCAGCC 920
 GGCCAAGCCGACCGACCGTGCCCAACCAGGTGCGGGTGATC 960
 TGCGGTAACGGGTGCGGCCGAGATCTGGGATGAGTTCA 1000
 1010 1020 1030 1040
 CCACCCGCTTCGGGGTCCGCGGGGTGTGCGAGTTCTACGC 1040
 CGCCAGCGAAGGCAACTCGGCCTTTATCAACATCTTCAAC 1080
 GTGCCCAGGACCGCCGGGGTATCGCCGATGCCGCTTGCTT 1120
 TTGTGGAATACGACCTGGACACCGGCGATCCGCTGCGGGA 1160
 TCGGAGCGGGCGAGTGCGTCGGGTACCCGACGGTGAACCC 1200

Fig. 88A

09405604 = 002399

Fig. 88B

mtFATP coding only.protein

10 20 30 40
MSDYYGGAHTTVRLIDLATRMPRVLADTPVIVRGAMTGLL 40
ARPNKASIGTVFQDRAARYGDRVFLKFGDQQLTYRDANA 80
TANRYAAVLAARGVGPGDVVGIMLRNSPSTVLAMLATVKC 120
GAIAGMLNYHQRGEVLAHSLGLLDAKVLIAESDLVSAVAE 160
CGASRGRVAGDVLTVEDVERFATTAPATNPASASAVQAKD 200
210 220 230 240
TAFYIFTSGTTGFPAKASVMTHHRWLRALAVFGGMGLRLKG 240
SDTLYSCLPLYHNNALTVAVSSVINSGATLALGKSFSASR 280
FWDEVIANRATAFVYIGEICRYLLNQPAKPTDRAHQVRVI 320
CGNGLRPEIWDEFTTRFGVARVCEFYAASEGNSAFINIFN 360
VPRTAGVSPMPLAFVEYDLDTGDPLRDASGRVRRVPDGEF 400
410 420 430 440
GLLLSRVNRLQPFDDGYTDPVASEKKLVRNAFRDGDWCFNT 440
GDVMSPOGMGHAADFVRLGDTFRWKGENVATTQVEAALAS 480
DQTVEECTVYGVQIPRTGGRAGMAAITLRAGAEFDGOALA 520
RTVYGHLPGYALPLFVRVVGSLAHTTTFKSRKVELRNQAY 560
GADIEDPLYVLGPDDEGYVPYYAEYPEEVSLGRRPQG. 598

Fig. 89

00405504 00550460

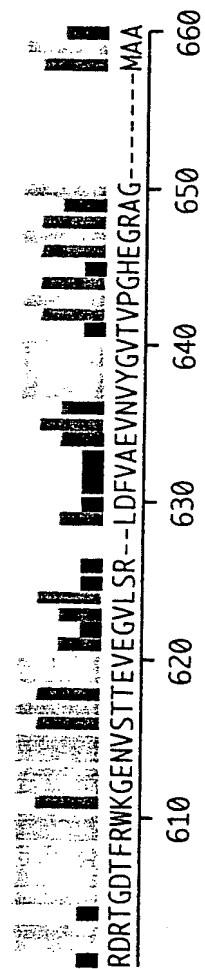
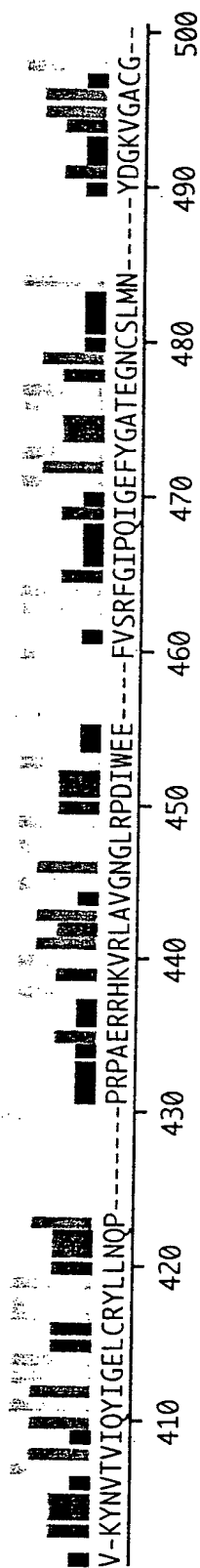
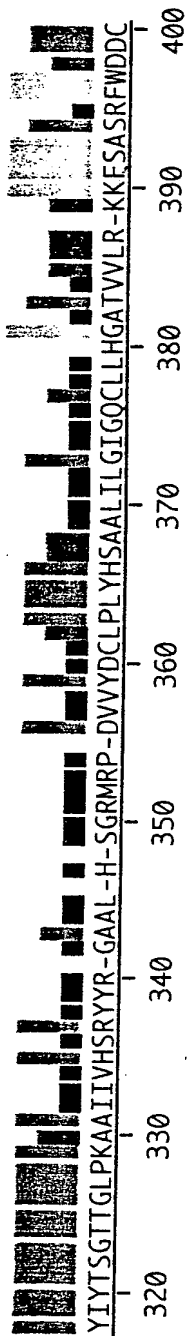


Figure 90

66E260" 10550460

hsVLACS full length protein

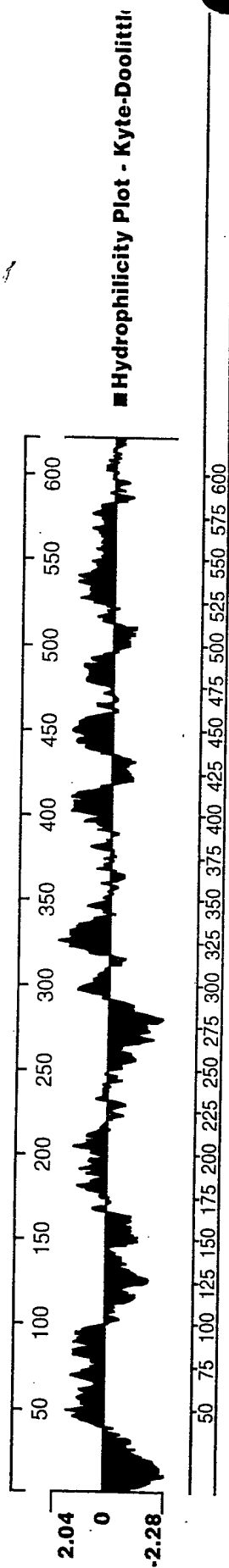


Figure 91

66260"40550460

hsFATP3partial.protein

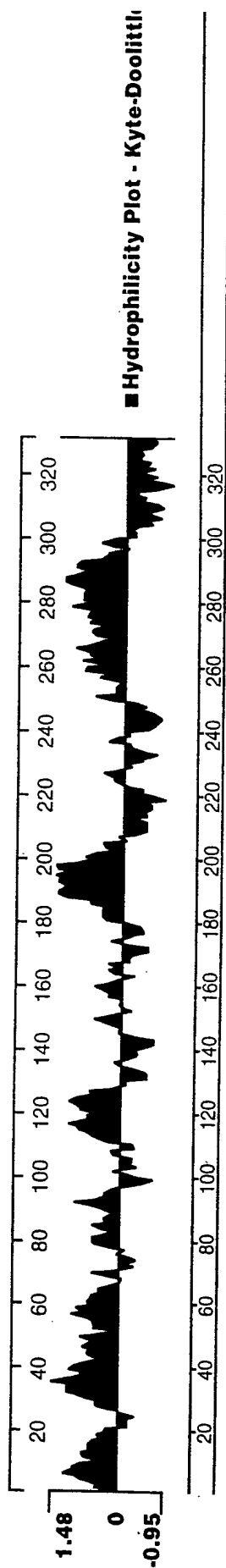


Figure 92

65E260" 405507150

hsFATP5partial.protein

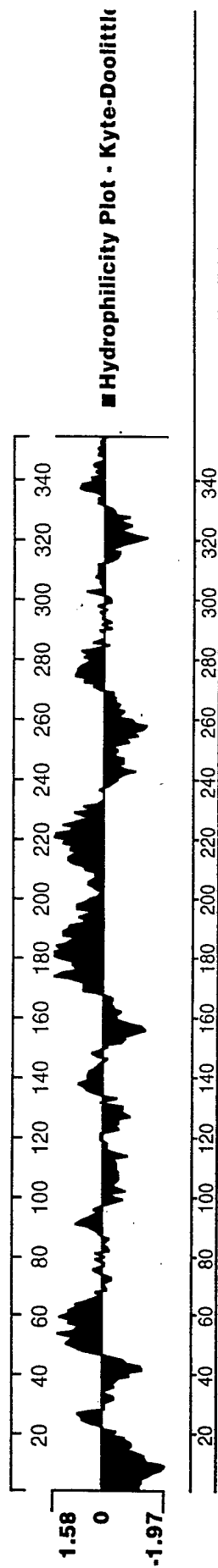


Figure 93

hsFATP3

```

1      cga ccc acg cgt ccg ggg atg ttt gcg agc ggc tgg aac cag acg gtg ccg ata gag gaa
1      M F A S G W N Q T V P I E E

61     gcg ggc tcc atg gct gcc ctc ctg ctg ctg ccc ctg ctg ctg ttg cta ccg ctg ctg ctg
15     A G S M A A L L L L P L L L L L P L L L

121    ctg ctg aag cta cac ctc tgg ccg cag ttg cgc tgg ctt ccg gcg gac ttg gcc ttt gcg
35     L L K L H L W P Q L R W L P A D L A F A

181    gtg cga gct ctg tgc tgc aaa agg gct ctt cga gct cgc gcc ctg gcc gcg gct gcc gcc
55     V R A L C C K R A L R A R A L A A A A A

241    gac ccg gaa ggt ccc gag ggg ggc tgc agc ctg gcc tgg cgc ctc gcg gaa ctg gcc cag
75     D P E G P E G G C S L A W R L A E L A Q

301    cag cgc gcc gcg cac acc ttt ctc att cac ggc tgc cgg cgc ttt agc tac tca gag gcg
95     Q R A A H T F L I H G S R R F S Y S E A

361    gag cgc gag agt aac agg gct gca cgc gcc ttc cta cgt gcg cta gcc tgg gac tgg gga
115    E R E S N R A A R A F L R A L G W D W G

421    ccc gac ggc ggc gac agc ggc gag ggg agc gct gga gaa ggc gag cgg gca gcg ccg gga
135    P D G G D S G E G S A G E G E R A A P G

481    gcc gga gat gca gcg gcc gga agc ggc gcg gag ttt gcc gga ggg gac ggt gcc gcc aga
155    A G D A A A G S G A E F A G G D G A A R

541    ggt gga gga gag ccc gcc gcc cct ctg tca cct gga gca act gtg gcg ctg ctc ctc ccc
175    G G G E P A A P L S P G A T V A L L L P

601    gct ggc cca gag ttt ctg tgg ctc tgg ttc ggg ctg gcc aag gcc gcc ctg cgc act gcc
195    A G P E F L W L W F G L A K A G L R T A

661    ttt gtg ccc acc gcc ctg cgc cgg ggc ccc ctg ctg cac tgc ctc cgc agc tgc ggc gcg
215    F V P T A L R R G P L L H C L R S C G A

721    cgc gcg ctg gtg ctg gcg cca gag ttt ctg gag tcc ctg gag ccg gac ctg ccc gcc ctg
235    R A L V L A P E F L E S L E P D L P A L

781    aga gcc atg ggg ctc cac ctg tgg gct gca ggc cca gga acc cac cct gct gga att agc
255    R A M G L H L W A A G P G T H P A G I S

841    gat ttg ctg gct gaa gtg tcc gct gaa gtg gat ggg cca gtg cca gga tac ctc tct tcc
275    D L L A E V S A E V D G P V P G Y L S S

901    ccc cag agc ata aca gac acg tgc ctg tac atc ttc acc tct ggc acc acg ggc ctc ccc
295    P Q S I T D T C L Y I F T S G T T G L P

961    aag gct gct cgg atc agt cat ctg aag atc ctg caa tgc cag ggc ttc tat cag ctg tgt
315    K A A R I S H L K I L Q C Q G F Y Q L C

1021   ggt gtc cac cag gaa gat gtg atc tac ctc gcc ctc cca ctc tac cac atg tcc ggt tcc
335    G V H Q E D V I Y L A L P L Y H M S G S

1081   ctg ctg ggc atc gtg ggc tgc atg ggc att ggg gcc aca gtg gtg ctg aaa tcc aag ttc
355    L L G I V G C M G I G A T V V L K S K F

1141   tgc gct ggt cag ttc tgg gaa gat tgc cag cag cac agg gtg acg gtg ttc cag tac att
375    S A G Q F W E D C Q Q H R V T V F Q Y I

1201   ggg gag ctg tgc cga tac ctt gtc aac cag ccc ccg agc aag gca gaa cgt ggc cat aag
395    G E L C R Y L V N Q P P S K A E R G H K

```

Figure 94A

09405504.092399

1261 gtc cgg ctg gca gtg ggc agc ggg ctg cgc cca gat acc tgg gag cgt ttt gtg cgg cgc
415 V R L A V G S G L R P D T W E R F V R R

1321 ttc ggg ccc ctg cag gtg ctg gag aca tat gga ctg aca gag ggc aac gtg gcc acc atc
435 F G P L Q V L E T Y G L T E G N V A T I

1381 aac tac aca gga cag cgg ggc gct gtg ggg cgt gct tcc tgg ctt tac aag cat atc ttc
455 N Y T G Q R G A V G R A S W L Y K H I F

1441 ccc ttc tcc ttg att cgc tat gat gtc acc aca gga gag cca att cgg gac ccc cag ggg
475 P F S L I R Y D V T T G E P I R D P Q G

1501 cac tgt atg gcc aca tct cca ggt gag cca ggg ctg ctg gtg gcc ccg gta agc cag cag
495 H C M A T S P G E P G L L V A P V S Q Q

1561 tcc cca ttc ctg ggc tat gct ggc ggg cca gag ctg gcc cag ggg aag ttg cta aag gat
515 S P F L G Y A G G P E L A Q G K L L K D

1621 gtc ttc cgg cct ggg gat gtt ttc ttc aac act ggg gac ctg ctg gtc tgc gat gac caa
535 V F R P G D V F F N T G D L L V C D D Q

1681 ggt ttt ctc cgc ttc cat gat cgt act gga gac acc ttc agg tgg aag ggg gag aat gtg
555 G F L R F H D R T G D T F R W K G E N V

1741 gcc aca acc gag gtg gca gag gtc ttc gag gcc cta gat ttt ctt cag gag gtg aac gtc
575 A T T E V A E V F E A L D F L Q E V N V

1801 tat gga gtc act gtg cca ggg cat gaa ggc agg gct gga atg gca gcc cta gtt ctg cgt
595 Y G V T V P G H E G R A G M A A L V L R

1861 ccc ccc cac gct ttg gac ctt atg cag ctc tac acc cac gtg tct gag aac ttg cca cct
615 P P H A L D L M Q L Y T H V S E N L P P

1921 tat gcc cgg ccc cga ttc ctc agg ctc cag gag tct ttg gcc acc aca gag acc ttc aaa
635 Y A R P R F L R L Q E S L A T T E T F K

1981 cag cag aaa gtt cgg atg gca aat gag ggc ttc gac ccc agc acc ctg tct gac cca ctg
655 Q Q K V R M A N E G F D P S T L S D P L

2041 tac gtt ctg gac cag gct gta ggt gcc tac ctg ccc ctc aca act gcc cgg tac agc gcc
675 Y V L D Q A V G A Y L P L T T A R Y S A

2101 ctc ctg gca gga aac ctt cga atc tga gaa ctt cca cac ctg agg cac ctg aga gag gaa
695 L L A G N L R I *

2161 ctc tgt

Figure 94B

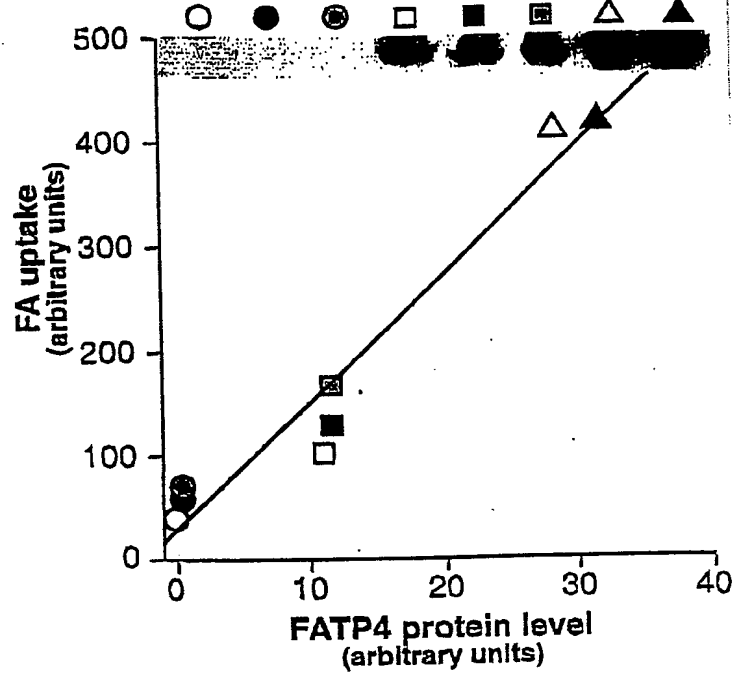


Figure 95

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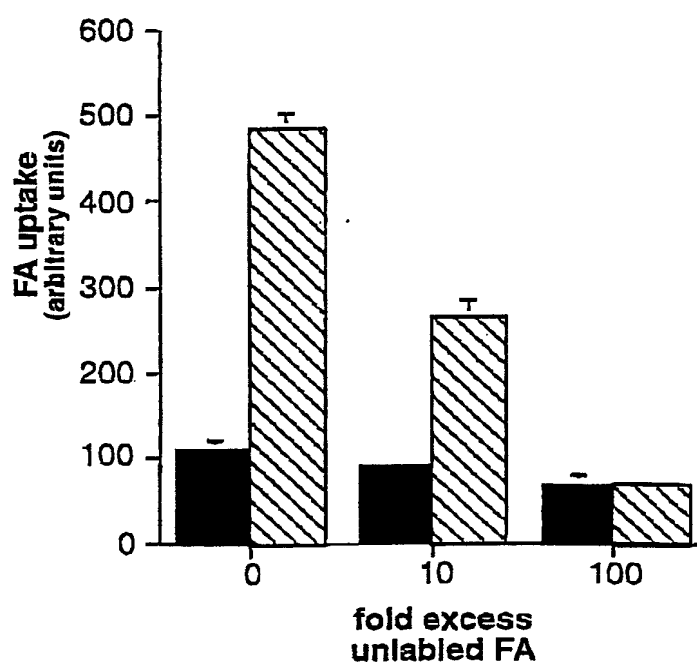


Figure 96

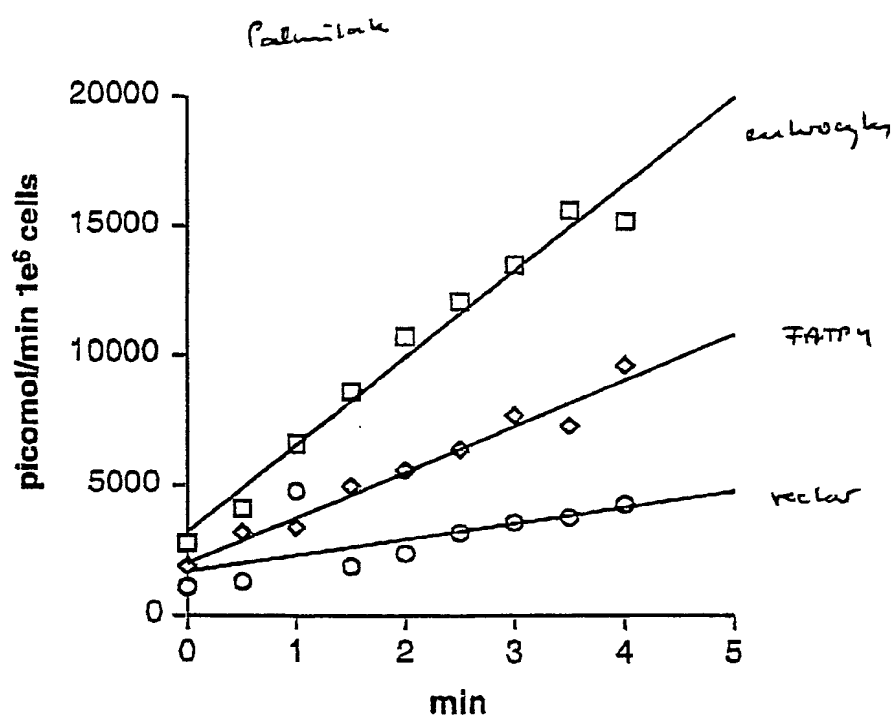


Figure 97

66260" 40550460

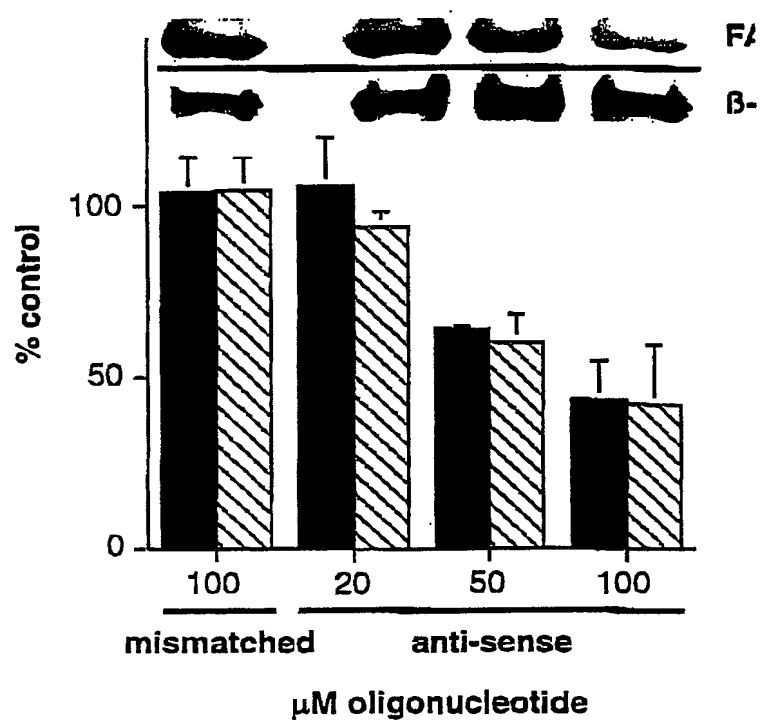


Figure 98

66E260" 40550460

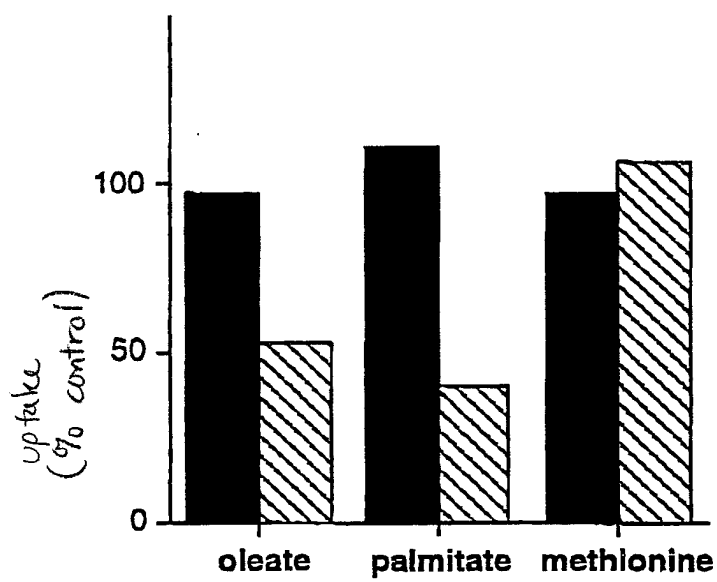


Figure 99